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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:05 ; Search time 11 Seconds
(without alignments)
94.264 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25

Sequence: 1 GWAALPRLIAFTSEHSFSLKKGAA 25

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1520

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 5 | 20.0 | 21 | 1 MISG MISAN | P81474 Misgurnus a |
| 2 | 5 | 20.0 | 24 | 1 FREA LITIN | P82023 litoria inf |
| 3 | 4 | 16.0 | 8 | 1 GLUR HUMAN | P02729 homo sapien |
| 4 | 4 | 16.0 | 19 | 1 ATPB CANFA | P99504 canis fami |
| 5 | 4 | 16.0 | 22 | 1 CUSP TRIVA | P3404 trichomonas |
| 6 | 4 | 16.0 | 23 | 1 ALLS HORSE | P82616 equus cabal |
| 7 | 4 | 16.0 | 23 | 1 FLAI SULSH | Q9UW96 sulfobus |
| 8 | 4 | 16.0 | 23 | 1 RR19 PETRY | P18550 petunia hyb |
| 9 | 4 | 16.0 | 24 | 1 PCW5 PACGO | P82427 pachycondyl |
| 10 | 3 | 12.0 | 8 | 1 CAD1 ENTEA | P13268 enterococcu |
| 11 | 3 | 12.0 | 8 | 1 LMT2 LOCM1 | P22396 locusta mig |
| 12 | 3 | 12.0 | 8 | 1 LFK LEUMA | P13049 leucophaea |
| 13 | 3 | 12.0 | 8 | 1 ORMY ORCLI | P82455 orconectes |
| 14 | 3 | 12.0 | 8 | 1 PKP2 PERAM | P82692 periplaneta |
| 15 | 3 | 12.0 | 8 | 1 PKP3 PERAM | P82618 periplaneta |
| 16 | 3 | 12.0 | 9 | 1 CCAP CARNA | P38556 carcinus ma |
| 17 | 3 | 12.0 | 9 | 1 LMT3 LOCM1 | P41489 locusta mig |
| 18 | 3 | 12.0 | 9 | 1 PKP1 PERAM | P82691 periplaneta |
| 19 | 3 | 12.0 | 10 | 1 ANGT CHICK | P01018 gallus gall |
| 20 | 3 | 12.0 | 10 | 1 GLEM HUMAN | P02728 homo sapien |
| 21 | 3 | 12.0 | 10 | 1 LPK2 LOCM1 | P41488 locusta mig |
| 22 | 3 | 12.0 | 10 | 1 UPA4 HUMAN | P30090 homo sapien |
| 23 | 3 | 12.0 | 11 | 1 CA42 LITCI | P82092 litoria cit |
| 24 | 3 | 12.0 | 11 | 1 LPW TETH | P05624 thermus the |
| 25 | 3 | 12.0 | 11 | 1 PKC1 CARMO | P82684 carausius m |
| 26 | 3 | 12.0 | 12 | 1 LMT1 LOCM1 | P22395 locusta mig |
| 27 | 3 | 12.0 | 12 | 1 LMT4 PERAM | P82619 periplaneta |
| 28 | 3 | 12.0 | 12 | 1 PKP4 PERU | P82690 periplaneta |
| 29 | 3 | 12.0 | 12 | 1 URZ2 FOLSP | P81022 polyodon sp |
| 30 | 3 | 12.0 | 13 | 1 CXA2 CONGE | P01520 conus geogr |
| 31 | 3 | 12.0 | 13 | 1 HPB9 RANES | P32416 rana esculi |
| 32 | 3 | 12.0 | 13 | 1 LMT4 LOCM1 | P41490 locusta mig |
| 33 | 3 | 12.0 | 14 | 1 CAL1 CALGI | P20728 calotropis |

| | | | | | |
|----|---|------|----|--------------|----------------------|
| 34 | 3 | 12.0 | 14 | 1 LPW SALTY | P03054 salmonella |
| 35 | 3 | 12.0 | 14 | 1 MAST PARID | P42716 parapolybia |
| 36 | 3 | 12.0 | 14 | 1 MAST VESLE | P01514 vespa lew |
| 37 | 3 | 12.0 | 14 | 1 MAST VESMA | P04205 vespa manda |
| 38 | 3 | 12.0 | 14 | 1 MAST VESOR | P17238 vespa orien |
| 39 | 3 | 12.0 | 14 | 1 MCRX METTM | P5815 methanobact |
| 40 | 3 | 12.0 | 14 | 1 MY14 EISFO | P46979 eisenia foe |
| 41 | 3 | 12.0 | 14 | 1 PPK6 PERAM | P82693 periplaneta |
| 42 | 3 | 12.0 | 14 | 1 SMS1 MYOSC | P20750 myoxocephal |
| 43 | 3 | 12.0 | 14 | 1 SMS ALLMI | P31985 alligator m |
| 44 | 3 | 12.0 | 15 | 1 ASPI LACSN | P82648 lactobacilli |
| 45 | 3 | 12.0 | 15 | 1 DIDH PSESP | P80701 pseudomonas |
| 46 | 3 | 12.0 | 15 | 1 HS11 PINPS | P81083 pinus pinas |
| 47 | 3 | 12.0 | 15 | 1 SODM STRGR | P80733 streptomyce |
| 48 | 3 | 12.0 | 16 | 1 CXA2 CONMA | P56636 conus magus |
| 49 | 3 | 12.0 | 16 | 1 FIBA MUSVI | P14458 mustela vis |
| 50 | 3 | 12.0 | 16 | 1 FOR1 MYRGU | P81438 myrmecia gu |
| 51 | 3 | 12.0 | 16 | 1 FOR2 MYRGU | P81437 myrmecia gu |
| 52 | 3 | 12.0 | 16 | 1 LPK1 LOCM1 | P20404 locusta mig |
| 53 | 3 | 12.0 | 16 | 1 RIPK TRIKI | P16093 trichosanthe |
| 54 | 3 | 12.0 | 16 | 1 UVSX BPT6 | Q06728 bacteriophage |
| 55 | 3 | 12.0 | 16 | 1 YMOR PSEPU | Q02210 pseudomonas |
| 56 | 3 | 12.0 | 17 | 1 APID BOMPA | P81464 bombus pasc |
| 57 | 3 | 12.0 | 17 | 1 FLA2 BARBA | P35634 bartonella |
| 58 | 3 | 12.0 | 17 | 1 MDH ACIDE | P80540 acidovorax |
| 59 | 3 | 12.0 | 17 | 1 PPK5 PERAM | P82617 periplaneta |
| 60 | 3 | 12.0 | 17 | 1 RN35 YEAST | P36530 saccharomyc |
| 61 | 3 | 12.0 | 17 | 1 YALA TRYBB | P17961 trypanosoma |
| 62 | 3 | 12.0 | 18 | 1 MU21 LITGE | P82068 litoria gen |
| 63 | 3 | 12.0 | 18 | 1 PHPT PSESE | P25971 pseudaletia |
| 64 | 3 | 12.0 | 19 | 1 MDH COMAC | P80539 comamonas a |
| 65 | 3 | 12.0 | 19 | 1 MDH SHEON | P82177 shewanella |
| 66 | 3 | 12.0 | 20 | 1 MDH KIBAR | P19978 kibdelospor |
| 67 | 3 | 12.0 | 20 | 1 MDH MICGL | P19979 microtetras |
| 68 | 3 | 12.0 | 20 | 1 PYR8 PYRAP | P37362 pyrrhocoris |
| 69 | 3 | 12.0 | 20 | 1 SB18 MAIZE | P82967 zea mays (m |
| 70 | 3 | 12.0 | 20 | 1 SODP PASPI | P81527 pasteurella |
| 71 | 3 | 12.0 | 20 | 1 UN05 PINPS | P81674 pinus pinas |
| 72 | 3 | 12.0 | 20 | 1 VMO2 CHICK | Q9P849 gallus gall |
| 73 | 3 | 12.0 | 20 | 1 VSP1 TRIOK | P20005 trimeresaur |
| 74 | 3 | 12.0 | 21 | 1 BOH1 BOMVA | P82282 bombina var |
| 75 | 3 | 12.0 | 21 | 1 BOH4 BOMVA | P82284 bombina var |

ALIGNMENTS

RESULT 1

| | | | |
|--|-----------|------|--------|
| MISG MISAN | STANDARD; | PRT; | 21 AA. |
| ID P81474; | | | |
| AC DT 15-DEC-1998 (Rel. 37, Created) | | | |
| DT 15-DEC-1998 (Rel. 37, Last sequence update) | | | |
| DE 15-DEC-1998 (Rel. 37, Last annotation update) | | | |
| DE Misgurnin. | | | |
| OS Misgurnus anguillicaudatus. | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC Actinopterygii; Neopterygii; Teleostei; Cypriniformes; | | | |
| OC Cobitidae; Misgurnus. | | | |
| OX NCBI_TaxID=75329; | | | |
| RN [1] | | | |
| RP SEQUENCE. | | | |
| RX MEDLINE=97415401; PubMed=9271200; | | | |
| RA Park C.B., Lee H.J., Park I.Y., Kim M.S., Kim S.C.; | | | |
| RT "A novel antimicrobial peptide from the loach, Misgurnus | | | |
| RL anguillicaudatus." | | | |
| CC - - FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST SEVERAL | | | |
| CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA AND FUNGI. | | | |
| CC - - MASS SPECTROMETRY: MW=2502; METHOD=MALDI. | | | |
| KW Antibiotic; Fungicide. | | | |
| SK SEQUENCE 21 AA, 2502 MW, 4A6E9D0AB391BCF1 CRC64; | | | |

Query Match 20.0%; Score 5; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGAA 25
 |||||
 Db 12 KKGAA 16

RESULT 2

ID_FRA4_LITIN STANDARD; PRT; 24 AA.
 AC P82023;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Frenatin 4.
 OS Litoria infrafrenata (Giant tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OC NCBI_TaxID=61195;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97368637; PubMed=9225251;
 RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "The structures of the frenatin peptides from the skin secretion of
 the giant tree frog Litoria infrafrenata.";
 RL J. Pept. Sci. 2:117-124(1996).
 CC -1- FUNCTION: WIDE SPECTRUM ANTIMICROBIAL PEPTIDE.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.
 CC -1- MASS SPECTROMETRY: MW=2493; METHOD=FAB.
 KW Antibiotic; Amphibian skin.
 SQ SEQUENCE 24 AA; 2495 MW; 6986D063947805A1 CRC64;

Query Match 20.0%; Score 5; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKGA 24
 |||||
 Db 6 LKGA 10

RESULT 3

ID_FLUR_HUMAN STANDARD; PRT; 8 AA.
 AC P02729;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urine glycopeptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72062338; PubMed=5126885;
 RA Lote C.J., Weiss J.B.;
 RT "Identification in urine of a low-molecular-weight highly polar
 glycopeptide containing cysteinyl-galactose.";
 RL Biochem. J. 123:25P-25P(1971).
 CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
 IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
 ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A
 SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
 DR PIR; A03188; XGHUEU.
 KW Glycoprotein.
 FT CARBOHYD 1 1 S-LINKED (GAL...);
 SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5BLEBIE CRC64;

Query Match 16.0%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 EHS 17
 |||||
 Db 2 EHS 5

RESULT 4

ID_ATPB_CANFA STANDARD; PRT; 19 AA.
 AC P99504;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ATP synthase beta chain, mitochondrial (EC 3.6.3.14) (Fragment).
 GN ATP5B.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
 CC SUBUNIT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
 DR HSC-2DPAGE; P99504; DOG.
 DR InterPro; IPR000194; ATPase a/bcentre.
 DR PROSITE; PS00152; ATPASE ALPHA BETA, PARTIAL.
 KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolyase; ATP-binding;
 KW Mitochondrion.
 FT UNSURE 8 8
 FT UNSURE 17 19
 FT NON TER 19 19
 SQ SEQUENCE 19 AA; 1871 MW; BB9C163FDC60BB42 CRC64;

Query Match 16.0%; Score 4; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGA 25
 |||||
 Db 9 KGA 12

RESULT 5

ID_CVSP_TRIVA STANDARD; PRT; 22 AA.
 AC P33404;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cysteine proteinase (EC 3.4.22.-) (Fragment).
 OS Trichomonas vaginalis.
 OC Eukaryota; Parabasalida; Trichomonadida; Trichomonadidae;
 OC Trichomonadinae; Trichomonas.
 OC NCBI_TaxID=5722;

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RN RP SEQUENCE.
RX MEDLINE=93307628; PubMed=8319888;
RA Irvine J.W., Coombs G.H., North M.J.,
RT "Purification of cysteine proteinases from trichomonads using
RT bacitracin-Sepharose.";
RL FEMS Microbiol. Lett. 110:113-120(1993).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR MEROPS, C01.082; -.
DR InterPro; IPR000169; SHprot acsite.
DR PROSITE; PS00139; THIOLESTERASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOLESTERASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOLESTERASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease.
FT UNSURE 1
FT NON_TER 22 22 OR K.
SQ SEQUENCE 22 AA; 2398 MW; 0EE40FDB6661ACBC CRC64;

Query Match 16.0%; Score 4; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KXGA 24
DB 9 KXGA 12

RESULT 6
ALL5 HORSE
ID ALL5 HORSE STANDARD; PRT; 23 AA.
AC P82616;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dander allergen Equ c 5 (Fragmente).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Hair dandruff;
RX MEDLINE=21257838; PubMed=11358533;
RA Goubard Botros H., Poncet P., Rabillon J., Fontaine T., Laval J.-M.,
RA David B.,
RT "Biochemical characterization and surfactant properties of horse
RT allergens.";
RL Eur. J. Biochem. 268:3126-3136(2001).
CC -|- SUBCELLULAR LOCATION: Secreted (Potential).
CC -|- MASS SPECTROMETRY: MW=16700; METHOD=Electrospray.
CC -|- MISCELLANEOUS: Allergen of horse dander. The determined pI of this
CC protein is 5.25.
KW Allergen.
FT NON_TER 1 1
FT NON_CONS 11 12
FT NON_TER 23 23
SQ SEQUENCE 23 AA; 2638 MW; 2406F19124582153 CRC64;

Query Match 16.0%; Score 4; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPRL 8
DB 9 LPRL 12

RESULT 7
FLA1 SULSH
ID FLA1 SULSH STANDARD; PRT; 23 AA.
AC Q9UWG6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 31/33 kDa flagellin (Fragment).
OS Sulfolobus shibatae.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2286;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 51178 / DSM 5389 / B12;
RX MEDLINE=96146545; PubMed=8550530;
RA Faguy D.M., Bayley D.P., Kostyukova A.S., Thomas N.A., Jarrell K.F.;
RT "Isolation and characterization of flagella and flagellin proteins
RT from the Thermocacidophilic archaea Thermoplasma volcanium and
RT Sulfolobus shibatae.";
RL J. Bacteriol. 178:902-905(1996).
CC -|- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF FLAGELLA.
CC -|- PTM: GLYCOSYLATED.
CC -|- SIMILARITY: BELONGS TO THE ARCHAEAL FLAGELLIN FAMILY.
KW Flagella; Glycoprotein.
FT NON_TER 23 23
SQ SEQUENCE 23 AA; 2362 MW; BB372157B44DB3AC CRC64;

Query Match 16.0%; Score 4; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIAP 11
DB 10 LIAP 13

RESULT 8
RR19_PETHY
ID RR19_PETHY STANDARD; PRT; 23 AA.
AC P18550;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 (Fragment).
GN RPS19.
OS Petunia hybrida (Petunia).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89136067; PubMed=3224388;
RA Aldrich J., Cherney B.W., Williams C., Merlin E.;
RT "Sequence analysis of the junction of the large single copy region
RT and the large inverted repeat in the petunia chloroplast genome.";
RL Curr. Genet. 14:487-492(1988).
CC -|- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -|- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M37322; AB02425.1; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; I.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding; Chloroplast.
FT INIT MET 0 0 BY SIMILARITY.
FT NON_TER 23 23

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SQ SEQUENCE 23 AA; 2665 MW; CA20D0128FC9AA49 CRC64;

Query Match 16.0%; Score 4; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22

DB 3 SLKK 6

RESULT 9

PCWS_PACGO STANDARD; PRT; 24 AA.

AC P82427;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ponericin W5.
OS achycondyla goeldii (Ponerine ant.).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Formicidae; Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;

RN [1]

RP SEQUENCE, AND FUNCTION.

RC TISSUE=Venom;

RX MEDLINE=21264562; PubMed=11279030;

RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,

RA Longeon A., Chafotte A., Dejean A., Rossier J.;

RT "Ponericins, new antibacterial and insecticidal peptides from the

RT venom of the ant pachycondyla goeldii.";

RL J. Biol. Chem. 276:17823-17829(2001).

CC -1- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE

CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL

CC AND HEMOLYTIC ACTIVITIES.

CC -1- MASS SPECTROMETRY: MW=2599.67; METHOD=WALDI.

KW Antibiotic; Insect immunity; Fungicide; Hemolysis.

SQ SEQUENCE 24 AA; 2600 MW; DDEBEACAA7D1D7E CRC64;

Query Match 16.0%; Score 4; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGAA 25

DB 7 KGAA 10

RESULT 10

CAD1_ENTFA

ID CAD1_ENTFA STANDARD; PRT; 8 AA.

AC P13268;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last annotation update)

DE Sex pheromone CAD1.

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI_TaxID=1351;

RN [1]

RP SEQUENCE.

RX MEDLINE=85051889; PubMed=6437872;

RA Mori M., Sagami Y., Narita M., Isogai A., Fujino M., Kitada C.,

RA Craig R.A., Clewell D.B., Suzuki A.,

RT "Isolation and structure of the bacterial sex pheromone, cad1, that

RT induces plasmid transfer in Streptococcus faecalis.";

RL FEBS Lett. 178:97-100(1984).

CC -1- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE

CC HEMOLYSIN PLASMID PAD1.

KW Pheromone.

SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20

DB 2 FSL 4

RESULT 11

LMT2_LOCFM

ID LMT2_LOCFM STANDARD; PRT; 8 AA.

AC P22396;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-AUG-1991 (Rel. 19, Last annotation update)

DE Locustamyotropin 2 (LOM-MT-2).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;

OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI_TaxID=7004;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;

RT "Isolation, identification and synthesis of locustamyotropin II, an

RT cephalomyotropic peptide family.";

RL Insect Biochem. 20:479-484(1990).

CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC (MYOTROPIC ACTIVITY).

CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD_RES 8 AMIDATION.

SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8

DB 6 PRL 8

RESULT 12

LPK_LEUMA

ID LPK_LEUMA STANDARD; PRT; 8 AA.

AC P13049;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Leukopyrokinin (LPK) (LEM-PK).

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;

OC Blaberoides; Blaberidae; Leucophaea.

OX NCBI_TaxID=6988;

RN [1]

RP SEQUENCE.

RX MEDLINE=86269041; PubMed=3015140;

RA Nachman R.J., Holman G.M., Cook B.J.;

RT "Active fragments and analogs of the insect neuropeptide

RT leukopyrokinin: structure-function studies.";

RL Biochem. Biophys. Res. Commun. 137:936-942(1986).

RN [2]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Head;

RX MEDLINE=87052651; PubMed=2877794;

RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of a blocked myotropic
 RT neuropeptide isolated from the cockroach, Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 85C:219-224(1986).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
 CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
 CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
 CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
 CC PENTAPEPTIDE FRAGMENT FTPL.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR PIR; A23967; A23967.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 92341771A9DSA1B6 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 6 PRL 8

RESULT 13
 ORMY ORCLI STANDARD; PRT; 8 AA.
 AC P82455;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Orcomyotropin (OMT).
 OS Orcomyotropin (OMT).
 CC Orcomyotropin (OMT).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 CC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 CC Astacidea; Astacoidea; Cambaridae; Orconectes.
 OX NCBI_TaxID=28379;
 RN [1]

SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.

RT TISSUE=Hindgut;
 EX MEDLINE=20411310; PubMed=10952880;
 RA Dirksen H., Burdick S., Sauter A., Keller R.;
 RT "Two orcomyotropins and the novel octapeptide orcomyotropin in the hindgut
 RT of the crayfish Orconectes limosus: identified myostimulatory
 RT neuropeptides originating together in neurons of the terminal
 RT abdominal ganglion.";
 RL J. Exp. Biol. 203:2807-2818(2000).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
 CC BY ABDOMINAL GANGLIONIC NEURONS.
 CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FA-B.
 KW Amidation; Neuropeptide.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 905 MW; 87661B1A9CDDA9 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 DB 3 APT 5

RESULT 14
 PPK2_PERAM STANDARD; PRT; 8 AA.
 AC P82652;
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 EX MEDLINE=97353923; PubMed=9210163;
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT retrocerebral complex of the American cockroach.";
 RL Peptides 18:473-478(1997).
 RN [2]
 RP TISSUE SPECIFICITY.
 RC MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 6 PRL 8

RESULT 15
 PPK3_PERAM STANDARD; PRT; 8 AA.
 AC P82678;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 EX MEDLINE=99212459; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 RT abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RC MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).

CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 ||||
 DB 6 PRL 8

RESULT 16
 CCAP CARMA STANDARD; PRT; 9 AA.
 AC 38556;
 DT J1-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cardioactive peptide (CCAP).
 OS Carcinus maenas (Common shore crab) (Green crab),
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
 OS Tenebrio molitor (Yellow mealworm), and
 OS Spodoptera eridania (Southern armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759, 7130, 7067, 37547;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.maenas; TISSUE=Pericardial organs;
 RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
 RT shore crab Carcinus maenas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=M.sexata;
 RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
 RT "Primary structure of a cardioactive neuropeptide from the tobacco
 RT hawkmoth, Manduca sexta.";
 RL FEBS Lett. 313:165-168 (1992).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
 RA Fuyua K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
 RA Schooley D.A.;
 RT "Isolation and identification of a cardioactive peptide from Tenebrio
 RT molitor and Spodoptera eridania.";
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
 CC INTO THE HEMOLYPH.
 DR PIR; A26363; A26363.
 DR PIR; S27233; S27233.
 KW Neuropeptide; Amidation.
 FT DISULFID 3
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 ||||
 DB 5 APT 7

RESULT 17
 LMT3_LOCMI STANDARD; PRT; 9 AA.
 ID P41489;
 AC P41489;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustamyotropin 3 (LOM-MT-3).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustamyotropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamyotropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452 (1992).
 CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 ||||
 DB 7 PRL 9

RESULT 18
 PPK1_PERAM STANDARD; PRT; 9 AA.
 ID P82691;
 AC P82691;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-1 (Pea-PK-1) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=97353923; PubMed=9210163;
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT reticerebral complex of the American cockroach.";
 RL Peptides 18:473-478 (1997).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;

Query Match 12.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 ||||
 DB 5 APT 7

CC -1- MASS SPECTROMETRY: MW=1010.4; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; PYROKININ.
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1011 MW; 885C176059C87DC1 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 7 PRL 9

RESULT 19

ANGT_CHICK STANDARD; PRT; 10 AA.
 AC F01018;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 DE (Fragment).
 GN AGT OR SERPINAS.
 OS Gallus gallus (Chicken), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031, 93934;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Chicken;
 RX MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sokabe H.;
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 RT angiotensin and its identification by DNS-method.",
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]

RP SEQUENCE.

RC SPECIES=C.C.japonica;
 RX MEDLINE=90284684; PubMed=2191893;
 RA Takei Y., Hasegawa Y.;
 RT "Vasopressor and depressor effects of native angiotensins and
 RT inhibition of these effects in the Japanese quail.",
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR; A01250; A01250.

DR PIR; A90917; A90917.

DR PIR; A60624; A60624.

DR InterPro; IPR000215; Serpin.

DR PROSITE; PS00284; SERPIN; PARTIAL.

KW Vasoconstrictor; Plasma; Serpin.

FT PEPTIDE 1 10 ANGIOTENSIN I.

FT PEPTIDE 1 8 ANGIOTENSIN II.

FT PEPTIDE 2 8 ANGIOTENSIN III.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1232 MW; CEFBD761F2DB42 CRC64;

Query Match

Best Local Similarity 12.0%; Score 3; DB 1; Length 10;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 DB 8 FSL 10

RESULT 20

GLEM_HUMAN STANDARD; PRT; 10 AA.
 AC P02728;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythrocyte membrane glycopeptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72034940; PubMed=5286858;
 RA Weiss J.B., Lote C.J., Bobinski H.;
 RT "New low molecular weight glycopeptide containing triglycosylcysteine
 RT in human erythrocyte membrane.",
 RL Nature New Biol. 234:25-26(1971).
 CC -1- PTM: S-LINKED GLYCAN CONSISTS OF GLC-GLC-GLC TRISACCHARIDE.
 CC -1- MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS
 CC PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
 CC ATTRIBUTED.

DR PIR; A03187; XGHUE.

KW Glycoprotein; Erythrocyte.

FT CARBOHYD 1 1 S-LINKED (GLC...).

SQ SEQUENCE 10 AA; 1049 MW; 239BFEEA1F5B18 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 HSH 17
 DB 4 HSH 6

RESULT 21

LFK2_LOCOMI STANDARD; PRT; 10 AA.
 AC P41488;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Locustapyrokinin 2 (LOM-PK-2) (FXPLR-amide).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Orthoptera; Orthopteroidea; Caelifera;

OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI_TaxID=7004;

RN [1]

RP SEQUENCE.

RC TISSUE=Brain;

RC MEDLINE=94094539; PubMed=7903606;

RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,

RA de Loof A.;

RT "Isolation, identification and synthesis of locustapyrokinin II from

RT Locusta migratoria, another member of the FXPLR-amide peptide

RT family.",

RL Comp. Biochem. Physiol. 106C:103-109(1993).

CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC

CC ACTIVITY).

CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAFA4271A9D1B772 CRC64;
Query Match 12.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
Db 8 PRL 10

RESULT 22
UPA4 HUMAN
ID UPA4 HUMAN STANDARD; PRT; 10 AA.
AC P30090;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE "known protein from 2D-page of plasma (Spot 12) (Fragment)."
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RC TISSUE=Plasma;
RX MEDLINE=9302937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Fisset J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8. ITS MW IS: 40.5 kDa.
CC -1- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30090; HUMAN.
FT NON TER 1 1
FT UNSURE 4 4
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;
Query Match 12.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TSE 14
Db 5 TSE 7

RESULT 23
CA42_LITCI
ID CA42_LITCI STANDARD; PRT; 11 AA.
AC P82092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Caerulein 4.2/4.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoides; Hylidae;
OC Pelodyadinae; Litoria.
CX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
mountains tree frog Litoria citropa. Part 1. Sequence determination

RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -1- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- PTM: ISOFORM 4.2Y4 DIFFERS FROM ISOFORM 4.2 IN NOT BEING
CC SULFATED.
CC -1- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian skin; Hypotensive agent; Amidation; Sulfation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;
Query Match 12.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SHF 18
Db 7 SHF 9

RESULT 24
LPW_THETH
ID LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-NOV-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL
OS Thermus thermophilus.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
CX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
HB8 trpE and trpG.";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRIPTOPHAN.
CC
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CC
CC EMBL; X07744; CAA30565.1; -
DR PIR; S03315; LFTWWE
KW Triptophan biosynthesis; Leader peptide.
SQ Triptophan biosynthesis; Leader peptide.
Query Match 12.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALP 6
Db 2 ALP 4

RESULT 25
PKC1_CARNO

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ID PKC1_CARMO STANDARD; PRT; 11 AA.
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Cam-PK-1) (FAPRL-Amide).
OS Carausius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatodea;
OC Heteronemidae; Carausius.
OX NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RA Predel R., Kellner R., Gaede G.;
RT "Myotropic neuropeptides from the retrocerebral complex of the stick
insect, Carausius morosus (Phasmatodea: Lonchodidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -|- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 6 PRL 8
DB 9 PRL 11

RESULT 26
LMT1_L0CMI STANDARD; PRT; 12 AA.
ID LMT1_L0CMI
AC P22395;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamyotropin.1 (LOM-WT-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90341077; PubMed=1974346;
RA Schoofs L., Holman G.M., Hayes T.K., Tips A., Nachman R.J.,
RA Vandesande F., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin
(Lom-WT), a novel biologically active insect peptide.";
RL Peptides 11:427-433(1990).
CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR FIR; A43975; A43975.
DR INTERPRO; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1213 MW; D766C92722D6DDDD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 PRL 8
DB 10 PRL 12

RESULT 27
PPK4_PERAM STANDARD; PRT; 12 AA.
ID PPK4_PERAM
AC P82619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (Pea-PK-4) (YXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RC MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -|- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -|- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAAL CRC64;

Query Match 12.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
DB 10 PRL 12

RESULT 28
PPK4_PERFU STANDARD; PRT; 12 AA.
ID PPK4_PERFU
AC P82690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (PFP-PK-4) (YXPRL-amide).
OS Periplaneta fuliginosa (Smokybrown cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=36977;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

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CC (-) MASS SPECTROMETRY; MW=1437.9; METHOD=WALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 CC InterPro: IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1439 MW; F9B53049FF42CAAL CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PRL 8
 Db 10 PRL 12
 RESULT 29
 UR LSP STANDARD; PRT; 12 AA.
 ID UR2 POLSP STANDARD; PRT; 12 AA.
 AC P81022;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin II (U-II) (UII).
 OS Polyodon spathula (North American paddlefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;
 OC Polyodon.
 OX NCBI_TaxID=7913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spinal cord;
 RX MEDLINE=96051494; PubMed=8536944;
 RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;
 RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
 RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon
 RT spathula).";
 RL Gen. Comp. Endocrinol. 99:323-332 (1995).
 CC -1- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
 CC MUSCLE STIMULATION.
 CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
 CC InterPro: IPR001483; Urotensin_II.
 DR Pfam; PF02083; Urotensin_II; 1.
 DR PROSITE; PS00984; UROTENSIN_II; 1.
 KW ornone.
 FT ISULFID 6 11 BY SIMILARITY.
 SQ SEQUENCE 12 AA; 1410 MW; 7551E9DBB879CEBB CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 TSE 14
 Db 3 TSE 5
 RESULT 30
 CX22 CONGE STANDARD; PRT; 13 AA.
 ID CX22 CONGE STANDARD; PRT; 13 AA.
 AC F01520;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin GII.
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN (1)

RP SEQUENCE.
 RX MEDLINE=81191854; PubMed=7014556;
 RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;
 RT "Peptide toxins from Conus geographus venom.";
 RL J. Biol. Chem. 256:4734-4740 (1981).
 RN (2)
 RP DISULFIDE BONDS.
 RX PubMed=6466616;
 RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,
 RA Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
 RA Cruz L.J., Rivier J.;
 RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of
 RT iodinated derivatives.";
 RL Biochemistry 23:2796-2802 (1984).
 CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PIR; A01783; NTKN2G.
 DR HSPSP; P56973; 1B45.
 DR Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 7
 FT DISULFID 3 13
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1422 MW; DBEE831C39297EBD CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 HFS 19
 Db 10 HFS 12
 RESULT 31
 HPB9 RANES STANDARD; PRT; 13 AA.
 ID HPB9 RANES STANDARD; PRT; 13 AA.
 AC P32416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Hemolytic protein B9 (Fragment).
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=8401;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90198965; PubMed=2317508;
 RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 RT extracts of Rana esculenta.";
 RL Biochim. Biophys. Acta 1033:318-323 (1990).
 CC -1- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: SKIN.
 DR PIR; S09019; S09019.
 KW Amphibian skin; Amidation; Hemolysis.
 FT MOD_RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIA 10
 DB 4 LIA 6

RESULT 32
 LMT4 LOCOMI
 ID LMT4 LOCOMI STANDARD; PRT; 13 AA.
 AC P41430.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustamytotropin 4 (LOM-MT-4).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda;
 OC Insecta, Pterygota, Neoptera, Orthopteroidea, Orthoptera, Caelifera;
 OC Acridomorpha, Acridoidea, Acrididae, Oedipodinae, Locusta.
 NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustamytotropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamytotropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE
 CC STIMULATOR THAN LOM-MT I, II AND III.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 13 13
 SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 11 PRL 13

RESULT 33
 CALI CALGI
 ID CALI CALGI STANDARD; PRT; 14 AA.
 AC P20728.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calotropin DI (EC 3.4.22.-) (Fragment).
 OS Calotropis gigantea (Madar) (Bowstring hemp).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asclepiadeae; Calotropis.
 OC Asclepiadeae; Calotropis.
 NCBI_TaxID=4066;
 RN [1]
 RP SEQUENCE.
 RA Bhattacharya D., Sengupta A., Sinha N.K.;
 RA "Chemical modification and amino terminal sequence of calotropin DI
 RT from Calotropis gigantea.";
 RL Phytochemistry 26:633-636(1987).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR PIR; PT0026; PT0026.
 DR MEROPS; C01.011;
 DR InterPro; IPR000169; SHprot_acsite.
 DR PROSITE; PS00139; THIOL PROTEASE CYS; PARTIAL.
 DR PROSITE; PS00639; THIOL PROTEASE HIS; PARTIAL.
 DR PROSITE; PS00640; THIOL PROTEASE ASN; PARTIAL.

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
 DB 1 MAA 3

KW Hydrolase; Thiol protease.
 FT MOD_RES 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1715 MW; D993F0276CDA4662 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGA 24
 DB 11 KGA 13

RESULT 34
 LPW SALTY
 ID LPW SALTY STANDARD; PRT; 14 AA.
 AC P03054;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Trp operon leader peptide.
 GN TRPL OR TRPEP OR STM1722.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OC NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=78196931; PubMed=351195;
 RA Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
 RT "Comparison of the nucleotide sequences of the initial transcribed
 RT regions of the tryptophan operons of Escherichia coli and Salmonella
 RT typhimurium.";
 RL J. Mol. Biol. 121:193-217(1978).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11577609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.

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DR EMBL; M24960; -; NOT ANNOTATED_CDS.
 DR EMBL; AE008776; AAL20640.1; -.
 DR PIR; A03590; LPEBWT.
 DR StyGene; SG10400; trpl.
 KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
 SQ SEQUENCE 14 AA; 1635 MW; 49F22A47362248E7 CRC64;

RESULT 35
MAST_PARIID STANDARD; PRT; 14 AA.
AC P42716; (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Mastoparan.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Polistinae; Parapolybia.
OX NCBI_TaxID=31921;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of
RT arapolybia indica."
RL Jisei Dobutsu 39:105-111(1988).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.
KW Mast cell degranulation; Venom; Amidation.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1619 MW; CA376CD3BA6D80DD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
|||
DB 6 MAA 8

RESULT 36
MAST_VESLE STANDARD; PRT; 14 AA.
AC P01514;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mastoparan.
OS Vespa lewisii (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7452;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RA MEDLINE=80155337; PubMed=540362;
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T., Fujino M., Kitada C.;
RT "A new mast cell degranulating peptide 'mastoparan' in the venom of
RT Vespa lewisii."
RL Chem. Pharm. Bull. 27:1942-1944(1979).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.
DR PIR; A01776; QMWAVV.
KW Mast cell degranulation; Venom; Amidation.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1480 MW; CC0C0EAC1D7B00DD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAL 5
|||
DB 7 AAL 9

RESULT 37
MAST_VESMA STANDARD; PRT; 14 AA.
AC P04205;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Mastoparan M (Mast cell-degranulating peptide).
OS Vespa mandarinia (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7446;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide, mastoparan-M, in the venom of
RT the hornet Vespa mandarinia."
RL Biomed. Res. 2:447-449(1981).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.

PIR; A01777; QMWMM.
DR Mast cell degranulation; Venom; Amidation.
KW Mast cell degranulation; Venom; Amidation.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1480 MW; C85N7EAC1D7B00DD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAL 5
|||
DB 7 AAL 9

RESULT 38
MAST_VESOR STANDARD; PRT; 14 AA.
AC P17238;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Mastoparan (Histamine releasing peptide I) (HR-I).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7447;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rozynov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet."
RL Bioorg. Khim. 7:1467-1477(1981).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.

PIR; JN0389; JN0389.
DR Mast cell degranulation; Venom; Amidation.
KW Mast cell degranulation; Venom; Amidation.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1494 MW; C84F9EAC026B00DD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAL 5
|||
DB 7 AAL 9

RESULT 39

MCRX METTM
ID MCRX METTM STANDARD; PRT; 14 AA.
AC P58615,
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase II alpha subunit (EC 1.8.-.-) (MCR II alpha) (Fragment).
GN MRTA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=91099370; PubMed=2269306;
RA Rospert S., Linder D., Ellermann J., Thauer R.K.;
RT "Two genetically distinct methyl-coenzyme M reductases in Methanobacterium thermoautotrophicum strain Marburg and delta H.";
RL Eur. J. Biochem. 194;871-877(1990).
CC -|- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)ethanesulfonic acid) with 7-mercaptoheptanoylthreonyl phosphate to methane and an heterodisulfide.
CC -|- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP = CH(4) + CoM-S-S-HTP.
CC -|- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY) TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL PORPHINOID.
CC -|- PATHWAY: Methanogenesis; last step.
CC -|- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
CC -|- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA. MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS CONTAINS MOSTLY MCR I.
KM Methanogenesis; Oxidoreductase; Multigene family.
FT NON-TER 14 14
SQ SEQUENCE 14 AA; 1718 MW; D317CCC562F00E29 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 LKK 22
DB 11 LKK 13

RESULT 40

MY14 EISFO
ID MY14 EISFO STANDARD; PRT; 14 AA.
AC P46979;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myosactive tetradecapeptide (ETP).
OS Eiseinia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida; Lumbricina; Lumbricidae; Eiseinia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Gut;
RX MEDLINE=96087879; PubMed=8532604;
RA Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H., Nomoto K.;
RA "A novel gut tetradecapeptide isolated from the earthworm, Eiseinia foetida.";
RT Peptides 16:995-999(1995).
RL Peptides 16:995-999(1995).
CC -|- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT MUSCLES.
CC -|- SIMILARITY: TO INSECTS ALLATOTROPIN.
KW Neuropeptide; Amidation.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1478 MW; CC9ABEF941CD91AD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
DB 5 GAA 7

RESULT 41

FPKG PERAM
ID FPKG PERAM STANDARD; PRT; 14 AA.
AC P82693;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-6 (Pea-PK-6) (FXPRK-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tissue-specific distribution of FXPRLamides in the nervous system of the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -|- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.
CC -|- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN ABDOMINAL PERISYPHATHETIC ORGANS.
CC -|- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.
CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinnin.
DR PROSITE; PS00539; PYROKINNIN; 1.
KW Amidation; Pyrokinnin.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1592 MW; 3966CC3FP384A998 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
DB 12 PRL 14

RESULT 42

SMS1 MYOSC
ID SMS1 MYOSC STANDARD; PRT; 14 AA.
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin 1.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Paddy sculpin), and Oncorhynchus kisutch (Coho salmon), and Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes; Cottoidae; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097, 8019, 7936;
RN [1]
RP SEQUENCE.
RC SPECIES=M. scorpius; TISSUE=Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkmer S., Thim L.;
RT "Structural characterization of peptides derived from

RT prosomatostatins I and II isolated from the pancreatic islets of two
 RT species of teleostean fish: the daddy sculpin and the flounder.";
 RL Eur. J. Biochem. 168:647-652(1987).
 RN [2]

RP SEQUENCE
 RC SPECIES=O.kisutch, TISSUE=Pancreas;
 RX MEDLINE=8705512; PubMed=2877919;
 RA Plietskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
 RA Kimmel J.R., Andrews P.C., Gorman A.;
 RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
 RT somatostatins";
 RL Gen. Comp. Endocrinol. 63:252-263(1986).
 RN [3]

RP SEQUENCE
 RC SPECIES=A.anguilla; TISSUE=Pancreas;
 RX MEDLINE=89065329; PubMed=2904391;
 RA Conlon J.M., Deacon C.F., Hazen N., Henderson I.W., Thim L.;
 RT "Somatostatins-related and glucagon-related peptides with unusual
 RT structural features from the European eel (Anguilla anguilla).";
 RI Gen. Comp. Endocrinol. 72:181-189(1988).
 CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

DR PIR, S00172; S00172.
 DR PIR, S00842; S00842.
 DR PIR, A60840; A60840.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Hormone; Multigene family.
 FT DISULFID 3 14
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTS 13
 Db 11 FTS 13

RESULT 43
 SMS_ALLMI STANDARD; PRT; 14 AA.
 AC P31885;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 06-OCT-2001 (Rel. 40, Last annotation update)
 DE somatostatin-14.
 OS Alligator mississippiensis (American alligator), and
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OC NCBI_TaxID=8496, 34903;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A.mississippiensis; TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 RN [2]

RP SEQUENCE.
 RC SPECIES=T. scripta;
 RX MEDLINE=90341082; PubMed=1974347;
 RA Conlon J.M., Hicks J.W.;
 RT "Isolation and structural characterization of insulin, glucagon and
 RT somatostatin from the turtle, Pseudemys scripta.";
 RL Peptides 11:461-466(1990).
 CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

DR PIR, C60414; C60414.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Hormone.
 FT DISULFID 3 14 BY SIMILARITY.
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTS 13
 Db 11 FTS 13

RESULT 44
 ASPI_LACSN STANDARD; PRT; 15 AA.
 ID ASPI_LACSN
 AC P82648;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acid shock protein 1 (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 CC Lactobacillus.
 OC NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CB1;
 RX MEDLINE=21322712; PubMed=11429463;
 RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobetti M.;
 RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
 RL Microbiology 147:1863-1873(2001).
 CC -!- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 23
 Db 3 KKG 5

RESULT 45
 DIDH_PSESP STANDARD; PRT; 15 AA.
 AC P80701;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD)
 DE (Hydroxyprostaglandin dehydrogenase) (HSD29) (Fragment).
 OS Pseudomonas sp.
 OC Bacteria; Proteobacteria.
 OC NCBI_TaxID=306;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97100200; PubMed=8944761;
 RA Oppermann U.C.T., Maser E.;
 RT "Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl
 RT reductase from the Gram-negative bacterium Comamonas testosteroni.";
 RL Eur. J. Biochem. 241:744-749(1996).
 CC -!- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND
 CC 3-OXO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED
 CC A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL
 CC COMPOUNDS, INCLUDING A METHYRONE-BASED CLASS OF INSECTICIDES, TO
 CC THE RESPECTIVE ALCOHOL METABOLITES.
 CC -!- CATALYTIC ACTIVITY: Androstosterone + NAD(P)(+) = 5-alpha-androstane-

3.17-dione + NAD(P)H.
 -1- SUBCELLULAR LOCATION: Cytoplasmic.
 -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 InterPro: IPR002198; ADH short.
 PROSITE: PS00061; ADH_SHORT; PARTIAL.
 Oxidoreductase; NAD.
 DOMAIN 6 >15 INVOLVED IN COFACTOR BINDING (BY SIMILARITY).
 NON TER 15 15
 SEQUENCE 15 AA; 1315 MW; 9506860D070AY790 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 GAA 25
 DB 13 GAA 15

RESULT 46
 HS11_PINPS STANDARD; PRT; 15 AA.
 AC P81083;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable class I heat shock protein (Water stress responsive protein 3) (Fragment).
 DE Pinus pinaster (Maritime pine).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RP TISSUE=Needle;
 RC MEDLINE=98418576; PubMed=9747804;
 RA Costa P., Bahman N., Frigerio J.-M., Kremer A., Plomion C.;
 RT "Water-deficit-responsive proteins in maritime pine."
 RL Plant Mol. Biol. 38:587-596(1998).
 RN [2]
 RP SEQUENCE.
 RP TISSUE=Needle;
 RC MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine proteins."
 RL Electrophoresis 20:1098-1108(1999).
 RN [3]
 RP REVISION TO 1.
 RA Frigerio J.-M.;
 RL Submitted (SEP-2001) to the SWISS-PROT data bank.
 CC -1- SUBUNIT: FORMS OLIGOMERIC STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- INDUCTION: BY WATER STRESS.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN (SPOT N144) IS: 6.1, ITS MW IS: 17 kDa.
 CC -1- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20) FAMILY.
 CC -1- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST AND CLASS IV WHICH IS IN THE ENOMEMERANE. THIS PROTEIN BELONGS TO CLASS I.
 CC InterPro: IPR002068; Hsp20.
 DR PROSITE: PS01031; HSP20; PARTIAL.
 KW Heat shock; Multigene family.
 FT NON TER 15 15
 SEQUENCE 15 AA; 1847 MW; 87FC504C2EB1F2B7 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 PSL 20
 DB 5 PSL 7

RESULT 47
 SODM_STRGR STANDARD; PRT; 15 AA.
 ID SODM_STRGR
 AC P80733;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
 DE SOD2.
 GN Streptomyces griseus.
 OS Streptomyces griseus.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE.
 RP STRAIN=KCTC 9006;
 RX MEDLINE=97056064; PubMed=8900409;
 RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
 RA Kang S.-O.;
 RT "Unique isozymes of superoxide dismutase in Streptomyces griseus."
 RL Arch. Biochem. Biophys. 334:341-348(1996).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Iron and zinc.
 CC -1- SUBUNIT: Tetramer.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 DR PROSITE: PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Iron; Zinc.
 FT NON TER 15 15
 SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 AAL 5
 DB 13 AAL 15

RESULT 48
 CXA2_CONMA STANDARD; PRT; 16 AA.
 ID CXA2_CONMA
 AC P56636;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin MII (M2).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RP TISSUE=Venom;
 RX MEDLINE=96205934; PubMed=8631783;
 RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
 RA McIntosh J.M.;
 RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptors."
 RL J. Biol. Chem. 271:7522-7528(1996).

[2] STRUCTURE BY NMR.
MEDLINE=98062282; PubMed=9398298;
Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
"three-dimensional solution structure of alpha-conotoxin MII, an
alpha2 neuronal nicotinic acetylcholine receptor-targeted
ligand";
Biochemistry 36:15693-15700(1997).
[3] STRUCTURE BY NMR.
MEDLINE=99060038; PubMed=9843366;
Hill J.M., Omen C.J., Miranda L.P., Bingham J.P., Alewood P.F.,
Craik D.J.;
"three-dimensional solution structure of alpha-conotoxin MII by NMR
spectroscopy: effects of solution environment on helicity";
Biochemistry 37:15621-15630(1998).
-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT
HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER
NACHR SUBUNIT COMBINATIONS.
-2- SUBCELLULAR LOCATION: Secreted.
-3- TISSUE SPECIFICITY: Expressed by the venom duct.
-4- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
FAMILY.
PDB: 1MII; 21-OCT-98.
PDB: 1M2C; 13-JAN-99.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation; 3D-structure.
DISULFID 2 8
DISULFID 3 16
MOD RES 16 16
SEQUENCE 16 AA; 1716 MW; 2822AF190166CAF9 CRC64;
Query Match 12.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 EHS 16
DB 11 EHS 13
RESULT 49
FIBR MUSVI STANDARD; PRT; 16 AA.
AC P14458;
DT 1-JAN-1990 (Rel. 13, Created)
DT 11-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.

FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16
SQ SEQUENCE 16 AA; 1679 MW; 09432A57919ECF66 CRC64;
Query Match 12.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 GAA 25
DB 12 GAA 14
RESULT 50
FOR1 MYRGU STANDARD; PRT; 16 AA.
AC P81438;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Formaein 1.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Formicidae; Myrmecinae; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph; PubMed=9497332;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible
O-glycosylated proline-rich antibacterial peptides.";
RL J. Biol. Chem. 273:6139-6143(1998).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E. COLI
BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
BACTERIA.
CC -1- INDUCTION: By bacterial infection.
CC -1- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
CC -1- SIMILARITY: TO DROSOPHILA DROSOCIN.
KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
FT CARBOHYD 11 11 O-LINKED (GALNAC...);
SQ SEQUENCE 16 AA; 1794 MW; 80CEA3AABBC2E0AE CRC64;
Query Match 12.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PRL 8
DB 14 PRL 16
RESULT 51
FOR2 MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Formaein 2.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Formicidae; Myrmecinae; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible

RT O-glycosylated proline-rich antibacterial peptides.";
 RL J. Biol. Chem. 273:6139-6143(1998).
 CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E. COLI
 CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
 CC BACTERIA.
 CC -|- INDUCTION: By bacterial infection.
 CC -|- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -|- SIMILARITY: TO DROSOPHILA DROSOCIN.
 CC Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 KW CARBOHYD 11 O-LINKED (GALNAC...)
 FT SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;
 SQ
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PRL 8
 DB 14 PRL 16
 RESULT 52
 LPK1 LOCM1 STANDARD; PRT; 16 AA.
 AC P20404;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustapyrokinin 1 (LOM-PK-1).
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Prorygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 CC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 CC NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=91224474; PubMed=2026322;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
 RT myotropic peptide of Locusta migratoria".
 RL Gen. Comp. Endocrinol. 81:97-104(1991).
 CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 CC PIR; A49761; A49761.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PRL 8
 DB 14 PRL 16
 RESULT 53
 RIPK1 TRIKI STANDARD; PRT; 16 AA.
 AC P1603;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein trichokirin (rRNA N-glycosidase)
 DE (EC 3.2.2.22) (Fragment).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eusoids 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=89005108; PubMed=3262509;
 RA Casellas P., Dussosoy D., Falaesca A.I., Barbieri L., Stirpe F.;
 RA Guillemot J.C., Ferrara P., Bolognesi A., Cenini P., Stirpe F.;
 RT trichokirin, a ribosome-inactivating protein from the seeds of
 RT Trichosanthes kirilowii Maximowicz. Purification, partial
 RT characterization and use for preparation of immunotoxins.";
 RL Eur. J. Biochem. 176:581-588(1988).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -|- PTM: GLYCOSYLATED.
 CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC PIR; S01669; S01669.
 DR InterPro; IPR001574; RIP.
 DR PROSITE; PS00275; SHIGA_RICIN; PARTIAL.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
 KW Glycoprotein.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1605 MW; 5E268A7F345935A2 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 FSL 20
 DB 4 FSL 6
 RESULT 54
 UVSX BPT6 STANDARD; PRT; 16 AA.
 ID UVSX BPT6
 AC Q06728;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Recombination and repair protein (Fragment).
 CC UVSX
 GN Bacteriophage T6.
 CC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 CC T4-like viruses.
 CC NCBI_TaxID=10666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93219141; PubMed=8464751;
 RA Winkler M., Rueger W.;
 RT "Cloning and sequencing of the genes of
 RT beta-glucosyl-HMC-alpha-glucosyl-transferases of bacteriophages T2
 RT and T6".
 RL Nucleic Acids Res. 21:1500-1500(1993).
 CC -|- FUNCTION: IMPORTANT IN GENETIC RECOMBINATION, DNA REPAIR, AND
 CC REPLICATION. POSSESSES PAIRING AND STRAND-TRANSFER ACTIVITY.
 CC INTERACTS WITH DDA AND GENE 32 PROTEINS.
 CC -|- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC EMBL; X68725; CAA48668.1;
 DR PIR; S35627; S35627.
 KW DNA damage; DNA replication; DNA recombination; DNA repair;

KW ATP-binding. 16 16
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1721 MW; 48164C95D76F3CB4 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLI 9
 Db 9 RLI 11

RESULT 55
 YNOR_PSEPU STANDARD; PRT; 16 AA.
 AC Q02210;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 06-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in MORA 3 region (Fragment).
 OS Pseudomonas putida.
 OG Plasmid pMDH7.2.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M10;
 RX MEDLINE=93119531; PubMed=8452544;
 RA Willey D.L., Caswell D.A., Lowe C.R., Bruce N.C.;
 RT "Nucleotide sequence and over-expression of morphine dehydrogenase, a
 RL plasmid-encoded gene from Pseudomonas putida M10.";
 RL Biochem. J. 290:539-544(1993).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M94775; AAB17357.1; -
 DR PIR; S30384; S30384.
 KW Hypothetical protein; Plasmid.
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1962 MW; A2F1EB8C172766ED CRC64;

Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPR 7
 Db 6 LPR 8

Search completed: December 19, 2002, 17:42:25
 Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:06 / Search time 28 Seconds
(without alignments)
183.971 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25

Sequence: 1 GWAALPRLIAPTSEHSFLKKGAA 25

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9297

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database :

SPTRMBL 21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_nhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-----------|--------------------|
| 1 | 6 | 24.0 | 10 | 5 QSWPE7 | Qswpe7 skogsbergia |
| 2 | 5 | 20.0 | 24 | 8 QSHG7 | Qshg7 chamaeleo h |
| 3 | 5 | 20.0 | 25 | 11 Q63999 | Q63999 rattus sp. |
| 4 | 5 | 20.0 | 25 | 11 Q64000 | Q64000 rattus sp. |
| 5 | 5 | 20.0 | 25 | 16 Q26056 | Q26056 helicobacte |
| 6 | 4 | 16.0 | 6 | 10 P82541 | P82541 spinacia ol |
| 7 | 4 | 16.0 | 8 | 2 Q56429 | Q56429 thermus the |
| 8 | 4 | 16.0 | 8 | 8 Q36898 | Q36898 nicotiana p |
| 9 | 4 | 16.0 | 9 | 5 Q9VV82 | Q9VV82 drosophila |
| 10 | 4 | 16.0 | 10 | 12 Q9347 | Q9347 hepatitis g |
| 11 | 4 | 16.0 | 12 | 10 P94011 | P94011 arabidopsis |
| 12 | 4 | 16.0 | 13 | 8 Q33417 | Q33417 digitalis p |
| 13 | 4 | 16.0 | 15 | 8 Q37016 | Q37016 nicotiana a |
| 14 | 4 | 16.0 | 16 | 8 Q36789 | Q36789 solanum nig |
| 15 | 4 | 16.0 | 18 | 4 Q16167 | Q16167 homo sapien |
| 16 | 4 | 16.0 | 18 | 5 Q26833 | Q26833 trypanosoma |

| | | | | | |
|----|---|------|----|-----------|--------------------|
| 17 | 4 | 16.0 | 19 | 2 Q9R4A3 | Q9r4a3 escherichia |
| 18 | 4 | 16.0 | 19 | 3 Q9UR87 | Q9ur87 candida par |
| 19 | 4 | 16.0 | 19 | 4 Q9UCE4 | Q9uce4 homo sapien |
| 20 | 4 | 16.0 | 19 | 8 Q36925 | Q36925 nicotiana v |
| 21 | 4 | 16.0 | 20 | 1 Q9UWJ2 | Q9uwj2 methanospir |
| 22 | 4 | 16.0 | 20 | 8 Q36584 | Q36584 nicotiana g |
| 23 | 4 | 16.0 | 23 | 8 Q36806 | Q36806 solanum tub |
| 24 | 4 | 16.0 | 24 | 8 Q8SKJ1 | Q8skj1 furcifer ca |
| 25 | 4 | 16.0 | 24 | 8 Q8SHJ1 | Q8shj1 chamaeleo c |
| 26 | 4 | 16.0 | 24 | 8 Q8SHI8 | Q8shi8 chamaeleo c |
| 27 | 4 | 16.0 | 24 | 8 Q8SHA7 | Q8sha7 brookesia a |
| 28 | 4 | 16.0 | 24 | 8 Q8SHA4 | Q8sha4 brookesia b |
| 29 | 4 | 16.0 | 24 | 8 Q8SH98 | Q8sh98 brookesia p |
| 30 | 4 | 16.0 | 24 | 8 Q8SH95 | Q8sh95 brookesia p |
| 31 | 4 | 16.0 | 24 | 8 Q8SH92 | Q8sh92 brookesia s |
| 32 | 4 | 16.0 | 24 | 8 Q8SH89 | Q8sh89 brookesia t |
| 33 | 4 | 16.0 | 24 | 8 Q8SH87 | Q8sh87 brookesia t |
| 34 | 4 | 16.0 | 24 | 8 Q8SH84 | Q8sh84 brookesia t |
| 35 | 4 | 16.0 | 24 | 10 Q9AUE9 | Q9aue9 brassica na |
| 36 | 4 | 16.0 | 24 | 13 P82833 | P82833 rana berla |
| 37 | 4 | 16.0 | 24 | 13 P82834 | P82834 rana berla |
| 38 | 4 | 16.0 | 24 | 13 P82838 | P82838 rana berla |
| 39 | 4 | 16.0 | 25 | 4 Q96F56 | Q96f56 homo sapien |
| 40 | 4 | 16.0 | 25 | 15 Q85452 | Q85452 moloney mur |
| 41 | 3 | 12.0 | 7 | 12 Q66113 | Q66113 cherry leaf |
| 42 | 3 | 12.0 | 8 | 2 O09258 | O09258 synechococc |
| 43 | 3 | 12.0 | 8 | 2 Q9AGP4 | Q9agp4 arthrobacte |
| 44 | 3 | 12.0 | 8 | 3 P82858 | P82858 puccinia re |
| 45 | 3 | 12.0 | 8 | 11 Q9ERD2 | Q9erd2 mus musculu |
| 46 | 3 | 12.0 | 8 | 11 Q9QVK5 | Q9qvk5 rattus sp. |
| 47 | 3 | 12.0 | 9 | 2 Q9R7H9 | Q9r7h9 haemophilus |
| 48 | 3 | 12.0 | 9 | 4 Q14277 | Q14277 homo sapien |
| 49 | 3 | 12.0 | 9 | 5 Q9TWV0 | Q9twv0 anthopleura |
| 50 | 3 | 12.0 | 9 | 6 Q9TRW2 | Q9trw2 oryctolagus |
| 51 | 3 | 12.0 | 9 | 10 Q988J8 | Q988j8 oryza sativ |
| 52 | 3 | 12.0 | 9 | 11 Q88889 | Q88889 mus musculu |
| 53 | 3 | 12.0 | 9 | 12 Q90350 | Q90350 hepatitis g |
| 54 | 3 | 12.0 | 9 | 12 Q9E1U7 | Q9e1u7 hepatitis b |
| 55 | 3 | 12.0 | 10 | 2 Q9X533 | Q9x533 escherichia |
| 56 | 3 | 12.0 | 10 | 2 Q9X534 | Q9x534 leclercia a |
| 57 | 3 | 12.0 | 10 | 2 Q9F5W1 | Q9f5w1 vibrio chol |
| 58 | 3 | 12.0 | 10 | 2 Q9AE19 | Q9ae19 streptococc |
| 59 | 3 | 12.0 | 10 | 2 Q60194 | Q60194 spiroplasma |
| 60 | 3 | 12.0 | 10 | 2 P83154 | P83154 anabaena sp |
| 61 | 3 | 12.0 | 10 | 3 Q8TG88 | Q8tg88 pleurotus o |
| 62 | 3 | 12.0 | 10 | 4 Q9H3R9 | Q9h3r9 homo sapien |
| 63 | 3 | 12.0 | 10 | 8 Q9T2P3 | Q9t2p3 rattus sp. |
| 64 | 3 | 12.0 | 10 | 8 Q8SHP0 | Q8shp0 bradypodion |
| 65 | 3 | 12.0 | 10 | 8 Q8SHM2 | Q8shm2 calumma boe |
| 66 | 3 | 12.0 | 10 | 8 Q8SHL3 | Q8shl3 calumma fur |
| 67 | 3 | 12.0 | 10 | 8 Q8SHL0 | Q8shl0 calumma gas |
| 68 | 3 | 12.0 | 10 | 8 Q8SHK1 | Q8shk1 calumma nas |
| 69 | 3 | 12.0 | 10 | 10 Q41788 | Q41788 zea mays (m |
| 70 | 3 | 12.0 | 10 | 11 Q9QVK8 | Q9qvk8 mus sp. mep |
| 71 | 3 | 12.0 | 10 | 12 P90373 | P90373 pseudorabie |
| 72 | 3 | 12.0 | 10 | 15 Q75595 | Q75595 human immun |
| 73 | 3 | 12.0 | 11 | 2 Q9S618 | Q9s618 prochloroco |
| 74 | 3 | 12.0 | 11 | 2 Q47451 | Q47451 escherichia |
| 75 | 3 | 12.0 | 11 | 2 P77404 | P77404 escherichia |

ALIGNMENTS

| RESULT 1 | QSWPE7 | PRELIMINARY; | PRT; | 10 AA. |
|----------|---|--------------|------|--------|
| QSWPE7 | QSWPE7 | | | |
| AC | QSWPE7 | | | |
| DT | 01-MAR-2002 (T-EMBLrel. 20, Created) | | | |
| DT | 01-MAR-2002 (T-EMBLrel. 20, Last sequence update) | | | |
| DT | 01-MAR-2002 (T-EMBLrel. 20, Last annotation update) | | | |
| DE | Opeln (Fragment). | | | |
| OS | Skogsbergia lernerii. | | | |

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Ostracoda; Myodocopa;
 OX Myodocopa; Cypridinoida; Cypridinidae; Skogsbergia.
 RN [1]_TaxID=176979;
 RP SEQUENCE FROM N.A.
 RC TISSUE-ENTIRE ORGANISM;
 RA Oakley T.H., Huber D.R.;
 RT "Eye-specific expression of multiple opsin loci in ostracod
 crustaceans";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF353377; AAL37547.1; --
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1035 MW; 1F4B3117672DDDD4 CRC64;
 Query Match 24.0%; Score 6; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 3 AALPRL 8
 DB 4 AALPRL 9
 RESULT 2
 Q8SHG7 PRELIMINARY; PRT; 24 AA.
 ID Q8SHG7
 AC Q8SHG7
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN ND1.
 OS Chamaeleo hoehnelti.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylia; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
 OX NCBI_TaxID=179913;
 RN [1]_TaxID=179913;
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448752; AAL90536.1; --
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 24 AA; 2638 MW; A253FFAE30A281CA CRC64;
 Query Match 20.0%; Score 5; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 QY 2 MAALP 6
 DB 20 MAALP 24
 RESULT 3
 Q63999 PRELIMINARY; PRT; 25 AA.
 ID Q63999
 AC Q63999
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Vasopressin (Fragment).
 GN VASOPRESSIN, VP.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]_TaxID=10118;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94286576; PubMed=8016115;

RA Evans D.A., van der Kleij A.A., Sonnemans M.A., Burbach J.P.,
 RA van Leeuwen F.W.;
 RT "Frameshift mutations at two hotspots in vasopressin transcripts in
 post-mitotic neurons";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:6059-6063 (1994).
 DR EMBL; S71426; AAB31127.1; --
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2478 MW; 4D78687ACF623B59 CRC64;
 Query Match 20.0%; Score 5; DB 11; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 QY 3 AALPR 7
 DB 4 AALPR 8
 RESULT 4
 Q64000 PRELIMINARY; PRT; 25 AA.
 ID Q64000
 AC Q64000
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Vasopressin (Fragment).
 GN VASOPRESSIN, VP.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]_TaxID=10118;
 RP SEQUENCE FROM N.A.
 RA Evans D.A., van der Kleij A.A., Sonnemans M.A., Burbach J.P.,
 RA van Leeuwen F.W.;
 RT "Frameshift mutations at two hotspots in vasopressin transcripts in
 post-mitotic neurons";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:6059-6063 (1994).
 DR EMBL; S71427; AAB31128.1; --
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2455 MW; B1F1E5E4D310F237 CRC64;
 Query Match 20.0%; Score 5; DB 11; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 QY 3 AALPR 7
 DB 4 AALPR 8
 RESULT 5
 Q26056 PRELIMINARY; PRT; 25 AA.
 ID Q26056
 AC Q26056
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein HP1528.
 GN HP1528.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]_TaxID=210;
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 EX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness S.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.B., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen *Helicobacter*
 RT *pylori*.";
 RL Nature 388:539-547 (1997).
 DR EMBL; AEO00651; AAO08577.1; --
 DR TIGR; HPI528; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 25 AA; 3075 MW; 5080933A41CE396E CRC64;

Query Match 20.0%; Score 5; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKKG 23
 DB 13 SLKKG 17
 |||||

RESULT 6
 P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE Chloroplast 308 ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3352;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Kneblach K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RL J. Biol. Chem. 37:28455-28465 (2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
 CC -!- FORM IS THE MINOR BASIC FORM.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR002222; Ribosomal S19.
 DR Pfam; PF00203; Ribosomal S19; PARTIAL.
 DR PROSITE; PRO00975; RIBOSOMALS19; PARTIAL.
 DR PROSITE; PS00323; RIBOSOMAL S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 16.0%; Score 4; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKKG 22
 DB 3 SLKKG 6
 |||||

RESULT 7
 Q56429 PRELIMINARY; PRT; 8 AA.
 ID Q56429

AC Q56429;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE GAPDH (Fragment).
 OS Thermus thermophilus.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
 OC Thermaceae; Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB-8;
 RX MEDLINE=89025722; PubMed=3052437;
 RA Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.;
 RT "Nucleotide sequence of the phosphoglycerate kinase gene from the
 RT extreme thermophile, *Thermus thermophilus*.";
 RL Biochem. J. 254:509-517 (1988).
 DR EMBL; X12464; CAA31005.1; --
 FT NON TER
 SQ SEQUENCE 8 AA; 885 MW; 33C87333732C72B CRC64;

Query Match 16.0%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKG 23
 DB 4 LKKG 7
 |||||

RESULT 8
 Q36898 PRELIMINARY; PRT; 8 AA.
 AC Q36898;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE RPS19' protein (Fragment).
 GN RPS19'.
 OS Nicotiana glauca, and
 OS Nicotiana glauca (Bigelow's tobacco).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=49453; 4088;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
 RL Mol. Gen. Genet. 0:0-0 (1996).
 DR EMBL; Z71234; CAA94933.1; --
 DR EMBL; Z71225; CAA94921.1; --
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 977 MW; FD43333735A411A6 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKKG 22
 DB 4 SLKKG 7
 |||||

RESULT 9
 Q9VV82 PRELIMINARY; PRT; 9 AA.
 AC Q9VV82;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)
 DE CG18219 protein (Fragment).

CG18219.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Jurtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Casley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA LaSko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR_4BL; AE003526; AAF49437.1; -
 DR_1lyBase; FBgn0036647; CG18219.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 975 MW; F31AB4472045B9C1 CRC64;

Query Match 16.0%; Score 4; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred.No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SHFS 19
 DB 1 SHFS 4

RESULT 10
 O90347 ID O90347 PRELIMINARY; PRT; 10 AA.
 AC O90347;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis G virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC GBV-C/HGV group.

OX NCBI_TaxID=45255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SG3332;
 RA Wong J., Chan S.H., Ren E.C.;
 RT "HGV isolates from Singapore: Evidence for novel Asian variants."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF078058; AAC32365.1; -
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1101 MW; 64FE2E672DC5A774 CRC64;

Query Match 16.0%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred.No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALPR 7
 DB 6 ALPR 9

RESULT 11
 P94011 ID P94011 PRELIMINARY; PRT; 12 AA.
 AC P94011;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Elongation factor EF-1 alpha A4 (Fragment).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GREEN SILIQUES OF A THALIANA ECOTYPE COLUMBIA;
 RA Raynal M., Grillet P., Laudie M., Meyer Y., Cooke R., Delseeny M.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z27066; CAA81582.1; -
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1229 MW; CEDA9EA59422CDD CRC64;

Query Match 16.0%; Score 4; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred.No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
 DB 8 KKGA 11

RESULT 12
 Q33417 ID Q33417 PRELIMINARY; PRT; 13 AA.
 AC Q33417;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Rps19, protein (Fragment).
 GN Rps19.
 OS Digitalis purpurea (Common foxglove).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Veronicaceae; Digitalis.
 OX NCBI_TaxID=4164;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96397499; PubMed=8804393;
 RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
 RT "Ebb and Flow of the Chloroplast Inverted Repeat."
 RL Mol. Genet. 252:195-206(1996).
 DR EMBL; Z71251; CAA94968.1; -

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KW Chloroplast. 13
FT NON TER 13
SQ SEQUENCE 13 AA; 1518 MW; 4D775A09A5SD4333 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 13
Q37016 PRELIMINARY; PRT; 15 AA.
ID Q37016
AC Q37016;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE RPS19, protein (Fragment).
GN RPS19.
OS Nicotiana glauca (Winged tobacco) (Persian tobacco),
OS Nicotiana glauca (Common tobacco), and
OS Nicotiana glauca (Tobacco).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4087, 4097, 35889;
RN [1]
RP SEQUENCE FROM N.A.
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RL Mol. Gen. Genet. 0:0-0(1996).
DR EMBL; Z71239; CAA94944.1; -
DR EMBL; Z71236; CAA94937.1; -
DR EMBL; Z71238; CAA94942.1; -
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
KW Chloroplast. 15
FT NON TER 15
SQ SEQUENCE 15 AA; 1756 MW; 09DE1D775A138C5D CRC64;

Query Match 16.0%; Score 4; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 14
Q36789 PRELIMINARY; PRT; 16 AA.
ID Q36789
AC Q36789;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Rps19, protein (Fragment).
GN Rps19.
OS Solanum nigrum (Black nightshade).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4112;
RN [1]
RP SEQUENCE FROM N.A.
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RL "Ebb and Flow of the Chloroplast Inverted Repeat.";
Mol. Gen. Genet. 252:195-206(1996).

DR Chloroplast. 13
FT NON TER 13
SQ SEQUENCE 13 AA; 1518 MW; 4D775A09A5SD4333 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 15
Q16167 PRELIMINARY; PRT; 18 AA.
ID Q16167
AC Q16167;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Serum albumin (Fragment).
GN SERUM ALBUMIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Madlison J., Galliano M., Watkins S., Minchiotti L., Porta F.,
RA Rossi A., Putnam F.W.;
RT "Genetic variants of human serum albumin in Italy: point mutants and a
RT carboxyl-terminal variant.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:6476-6480(1994).
DR EMBL; S70799; AAB31177.1; -
FT NON TER 1
SQ SEQUENCE 18 AA; 2089 MW; 2CCF6C5B0B08690B CRC64;

Query Match 16.0%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALPR 7
Db 3 ALPR 6

RESULT 16
Q26833 PRELIMINARY; PRT; 18 AA.
ID Q26833
AC Q26833;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Iatf 1.2) variant surface glycoprotein BC gene (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown K.H., Brentano S.T., Donelson J.E.;
RL "Mung bean nuclease cleaves preferentially at the boundaries of
variant surface glycoprotein gene transpositions in trypanosome DNA.";
J. Biol. Chem. 261:10352-10358(1986).
DR EMBL; M14021; AAA30306.1; -
FT NON TER 1
SQ SEQUENCE 18 AA; 2039 MW; 8EA0F51BD630BF8F CRC64;

Query Match 16.0%; Score 4; DB 5; Length 18;

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Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIAP 11
DB 11 LIAP 14

RESULT 17
Q9R4A3
ID Q9R4A3 PRELIMINARY; PRT; 19 AA.
AC Q9R4A3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE N-acetyl-D-NEURAMINIC acid lyase (EC 4.1.3.3) (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX 'CBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=96276413; PubMed=9694758;
RA Ferrero M.A., Reglero A., Fernandez-Lopez M., Ordas R.,
RA Rodriguez-Aparicio L.B.;
RT "N-acetyl-D-neuraminic acid lyase generates the sialic acid for
RT colominic acid biosynthesis in Escherichia coli K1."
RL Biochem. J. 317:157-165 (1996).
SQ SEQUENCE 19 AA; 2061 MW; 72022247A20EBBE3 CRC64;

Query Match 16.0%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAAL 5
DB 8 MAAL 11

RESULT 18
Q9UR87
ID Q9UR87 PRELIMINARY; PRT; 19 AA.
AC Q9UR87;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Class I cytochrome C isoform B (Fragment).
OS Candida parapsilosis (Yeast).
OC Ascomycota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5480;
RN [1]
RP SEQUENCE.
RX MEDLINE=93305688; PubMed=8391313;
RA Camougrand N., Velours J., Denis M., Guerin M.;
RA "Isolation, characterization and function of the two cytochromes c of
RT the yeast Candida parapsilosis."
RL Biochim. Biophys. Acta 1143:135-141 (1993).
SQ SEQUENCE 19 AA; 2108 MW; 17023D754FF25F87 CRC64;

Query Match 16.0%; Score 4; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
DB 10 KKGA 13

RESULT 19
Q9UCE4
ID Q9UCE4 PRELIMINARY; PRT; 19 AA.
AC Q9UCE4;

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DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE PROCATHEPSIN E (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93349047; PubMed=8346912;
RA Takeda-Ezaki M., Yamamoto K.;
RT "Isolation and biochemical characterization of procathepsin E from
RT human erythrocyte membranes."
RL Arch. Biochem. Biophys. 304:352-358 (1993).
SQ SEQUENCE 19 AA; 2293 MW; 3217ABB8670A65FC CRC64;

Query Match 16.0%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 12 SLKK 15

RESULT 20
Q36925
ID Q36925 PRELIMINARY; PRT; 19 AA.
AC Q36925;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE RPS19, protein (Fragment).
GN RPS19;
OS Nicotiana velutina,
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco), and
OS Nicotiana attenuata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=49454; 4092, 49451;
RN [1]
RP SEQUENCE FROM N.A.
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RL Mol. Gen. Genet. 0:0-0 (1996).
DR EMBL; Z71240; CAA94946.1; -
DR EMBL; Z71242; CAA94950.1; -
DR EMBL; Z71243; CAA94952.1; -
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; I.
KW Chloroplast.
FT NON TER
RP SEQUENCE 19 AA; 2239 MW; 19AA300AB9DE1D77 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 4 SLKK 7

RESULT 21
Q9UWJ2
ID Q9UWJ2 PRELIMINARY; PRT; 20 AA.
AC Q9UWJ2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE 35 kDa flagellin (Fragment).

```

OS Methanospirillum hungatei.
OC Archaea; Euryarchaeota; Methanococci; Methanomicrobiales;
OC Methanomicrobiaceae; Methanospirillum.
OX NCBI_TaxID=2203;
RN [1]
RP SEQUENCE.
RX MEDLINE=95095917; PubMed=8002572;
RA Faguy D.M., Koval S.F., Jarell K.F.;
RT "Physical characterization of the flagella and flagellins from
RT Methanospirillum hungatei.",
RL J. Bacteriol. 176:17491-7498 (1994).
SQ SEQUENCE 20 AA; 2036 MW; B2244BC7818F8799 CRC64;

Query Match 16.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 8 LIAP 11
Db 10 LIAP 13

RESULT 22

Q36584 PRELIMINARY; PRT; 20 AA.
ID Q36584
AC Q36584;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RPS19, protein (Fragment).
GN RPS19.
OS Nicotiana glauca (Glaucous tobacco) (Tree tobacco).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UNIV. OF BIRMINGHAM;
RX MEDLINE=96397499; PubMed=8804393;
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RT "Ebb and Flow of the Chloroplast Inverted Repeat.",
RL Mol. Gen. Genet. 252:195-206 (1996).
DR EMBL; Z71244; CAA94954.1; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
KW Chloroplast.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2398 MW; 2FC9AA300459DE1D CRC64;

Query Match 16.0%; Score 4; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 23

Q36806 PRELIMINARY; PRT; 23 AA.
ID Q36806
AC Q36806;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RPS19, protein (Fragment).
GN RPS19.
OS Solanum tuberosum (Potato).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96397499; PubMed=8804393;
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RT "Ebb and Flow of the Chloroplast Inverted Repeat.",
RL Mol. Gen. Genet. 252:195-206 (1996).
DR EMBL; Z71247; CAA94960.1; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
KW Chloroplast.
FT NON TER 23 23
SQ SEQUENCE 23 AA; 2709 MW; 9DD0128FC9AA300A CRC64;

Query Match 16.0%; Score 4; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 24

Q8SK10 PRELIMINARY; PRT; 24 AA.
ID Q8SK10
AC Q8SK10;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Furfifer campani.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Iguania; Acrodonta; Chamaeleonidae; Furfifer.
OX NCBI_TaxID=179925;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).",
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF487666; AAL90578.1; -.
DR Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 24 AA; 2588 MW; C95A0D19C55B81CB CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 AALP 6
Db 21 AALP 24

RESULT 25

Q8SHJ1 PRELIMINARY; PRT; 24 AA.
ID Q8SHJ1
AC Q8SHJ1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Chamaeleo calyptratus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OX NCBI_TaxID=179908;
RN [1]

RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448744; AAL90512.1; -
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2664 MW; A61DC2AE354791CA CRC64;
Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AALP 6
DB 21 AALP 24
RE 26
Q8 SHI8 PRELIMINARY; PRT; 24 AA.
AC Q8SHI8;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Chamaeleo chamaeleon.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OX NCBI_TaxID=91907;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448745; AAL90515.1; -
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2662 MW; B81C3D8D20F791CA CRC64;
Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AALP 6
DB 21 AALP 24
RESULT 27
Q8SH7 PRELIMINARY; PRT; 24 AA.
ID Q8SH7;
AC Q8SH7;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Brookesia antioetreae.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
OX NCBI_TaxID=179891;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF448773; AAL90599.1; -
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2652 MW; BD082475311691CA CRC64;
Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AALP 6
DB 21 AALP 24
RESULT 28
Q8SH4 PRELIMINARY; PRT; 24 AA.
ID Q8SH4;
AC Q8SH4;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Brookesia brygool.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
OX NCBI_TaxID=179892;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448774; AAL90602.1; -
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2596 MW; A22A1975310AEF2A CRC64;
Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AALP 6
DB 21 AALP 24
RESULT 29
Q8SH9 PRELIMINARY; PRT; 24 AA.
ID Q8SH9;
AC Q8SH9;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Brookesia perarmata.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
OX NCBI_TaxID=179894;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448776; AAL90608.1; -
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2652 MW; BD1701D6310AEF2A CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

RESULT 30

Q8SH95 PRELIMINARY; PRT; 24 AA.
 AC Q8SH95, 24 AA.
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Brookesia peyeriasi.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
 OC NCBI_TaxID=91904;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448777; AAL90611.1; -.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2654 MW; 9AF827BA3DF8A4D5 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

RESULT 31

Q8SH92 PRELIMINARY; PRT; 24 AA.
 AC Q8SH92, 24 AA.
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Brookesia superciliaris.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
 OC NCBI_TaxID=179895;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448778; AAL90614.1; -.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2562 MW; B22B1975311691CA CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6

RESULT 34

Db 21 AALP 24
 ||||

RESULT 32

Q8SH89 PRELIMINARY; PRT; 24 AA.
 AC Q8SH89, 24 AA.
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Brookesia therezieni.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
 OC NCBI_TaxID=179896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448779; AAL90617.1; -.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2560 MW; C95A197529B596BB CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

RESULT 33

Q8SH87 PRELIMINARY; PRT; 24 AA.
 AC Q8SH87, 24 AA.
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Brookesia thieli.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
 OC NCBI_TaxID=179897;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448780; AAL90620.1; -.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2622 MW; BD171975311691CA CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

Q8SH84
ID Q8SH84 PRELIMINARY; PRT; 24 AA.
AC Q8SH84;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Brookesia tuberculata.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
OX NCBI_TaxID=179898;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448781; AAL90623.1; -;
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2560 MW; C95A197529B596BB CRC64;
Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 AALP 6
Db 21 AALP 24
RESULT 35
Q9AUE9
ID Q9AUE9 PRELIMINARY; PRT; 24 AA.
AC Q9AUE9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Stearoyl-ACP desaturase (Fragment).
GN DELTA9-BN-1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DRAKKAR;
RA Fourmann M., Froger N., Brunel D.;
RT "Amplified consensus gene markers: Tools designing for a genetic map
of Arabidopsis known-function genes in Brassica.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF230689; AAK14946.1; -;
FT NON TER 1
FT NON TER 24
SQ SEQUENCE 24 AA; 2757 MW; 6C684EFD165113E0 CRC64;
Query Match 16.0%; Score 4; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 19 SLKK 22
Db 4 SLKK 7
RESULT 36
P82833
ID P82833 PRELIMINARY; PRT; 24 AA.
AC P82833;
DT 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Brevinin-1BA.
OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=30360;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop P.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
isolated from the skins of the North American frogs Rana luteiventris,
Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
S.AUREUS.
CC -|- MASS SPECTROMETRY: MW=2643; METHOD=ELECTROSPRAY.
CC -|- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
FAMILY.
KW Antibiotic.
FT DISULFID 18 24 BY SIMILARITY.
SQ SEQUENCE 24 AA; 2645 MW; CB524A454471DF4 CRC64;
Query Match 16.0%; Score 4; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GMAA 4
Db 7 GMAA 10
RESULT 37
P82834
ID P82834 PRELIMINARY; PRT; 24 AA.
AC P82834;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Brevinin-1BB.
OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=30360;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop P.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
isolated from the skins of the North American frogs Rana luteiventris,
Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
S.AUREUS AND GRAM-NEGATIVE BACTERIUM E.COLI. ACTIVE AGAINST
C.ALBICANS.
CC -|- MASS SPECTROMETRY: MW=2567.3; METHOD=ELECTROSPRAY.
CC -|- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
FAMILY.
KW Antibiotic; Fungicide.
FT DISULFID 18 24 BY SIMILARITY.
SQ SEQUENCE 24 AA; 2569 MW; CB524A454147DF4 CRC64;
Query Match 16.0%; Score 4; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GMAA 4
Db 7 GMAA 10


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Db 7 GMAA 10

RESULT 38
P82838 PRELIMINARY; PRT; 24 AA.
AC P82838;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE Brevinin-LBF.
OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=30360;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RT Rana berlandieri and Rana pipiens."
RL Eur. J. Biochem. 267:894-900(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S. AUREUS AND GRAM-NEGATIVE BACTERIUM E. COLI.
CC -!- MASS SPECTROMETRY: MW=2629, METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GABGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic.
FT DISULFID
SQ SEQUENCE 24 AA; 2631 MW; CB524A4544434CF4 CRC64;

Query Match 16.0%; Score 4; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAA 4
DB 7 GMAA 10

RESULT 39
Q96FS6 PRELIMINARY; PRT; 25 AA.
AC Q96FS6;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Unknown (protein for MGC:17410).
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010467; AAH10467.1; -.
SQ SEQUENCE 25 AA; 2768 MW; B06256B8661DAFC4 CRC64;

Query Match 16.0%; Score 4; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAAL 5
DB 1 MAAL 4

RESULT 40
Q85452 PRELIMINARY; PRT; 25 AA.
AC Q85452;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain 349) gag-mos splice junction mRNA
DE (Fragment).
OS Moloney murine leukemia virus.
OS Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85108156; PubMed=3982040;
RA Nash M.A., Brizzard B.L., Wong J.L., Murphy E.C.Jr.;
RT "Murine sarcoma virus ts110 RNA transcripts: Origin from a single
RT proviral DNA and sequence of the gag-mos junctions in both the
RT precursor and spliced viral RNAs."
RL J. Virol. 53:624-633(1985).
DR EMBL; K02856; AAA46489.1; -.
FT NON TER 25
SQ SEQUENCE 25 AA; 2668 MW; 3D1AF681EBF3B1C6 CRC64;

Query Match 16.0%; Score 4; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 HFSL 20
DB 17 HFSL 20

RESULT 41
Q66113 PRELIMINARY; PRT; 7 AA.
AC Q66113;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE C-terminus of the viral replicase (Fragment).
OS cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
RT strain).";
RL Virus Genes 10:245-252(1995).
DR EMBL; Z34265; CAA84019.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672BEDC6D740 CRC64;

Query Match 12.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPR 7
DB 5 LPR 7

RESULT 42
O09258

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Thu Dec 12 17:47:46 2002

RT "Exon structure and flanking intronic sequences of the human RET
 RT proto-oncogene.";
 RL Biochem. Biophys. Res. Commun. 196:1288-1295(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94366753; PubMed=8084609;
 RA Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
 RA Bocciaardi R., Nijveen H., Bolino A., Sari M., Ronchetto P., Pasini B.,
 RA Bazzano M., Buys C., Romeo G.
 RT "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
 the ret proto-oncogene";
 RL Oncogene 9:3025-3029(1994).
 DR EMBL; U11532; AAC50102.1; -.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;

Query Match 12.0%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 DB 5 APT 7

RESULT 49
 Q9TWVO PRELIMINARY; PRT; 9 AA.
 ID Q9TWVO PRELIMINARY; PRT; 9 AA.
 AC Q9TWVO; 2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
 DE Antho-RPAMIDE-NEUROPEPTIDE.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthese; Actinidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
 RT "Isolation of Leu-Pro-Gly-Pro-Arg-Pro-Arg-Pro-NH2 (Antho-RPamide),
 an N-terminally protected, biologically active neuropeptide from sea
 anemones";
 RL Peptides 13:851-857(1992).
 FT NON TER 1
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 12.0%; Score 3; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPR 7
 DB 6 LPR 8

RESULT 50
 Q9TRW2 PRELIMINARY; PRT; 9 AA.
 ID Q9TRW2 PRELIMINARY; PRT; 9 AA.
 AC Q9TRW2; 2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE CALDESMON=PHOSPHORYLATION site (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91378498; PubMed=1898046;
 RA Ikebe M., Hornick T.;
 RT "Determination of the phosphorylation sites of smooth muscle caldesmon

DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373341; PubMed=1832670;
 RA Hoppner W., Beckert L., Buck F., Seitz H.J.;
 RT "Is the p29 protein involved in the rapid regulation of
 phosphoenolpyruvate carboxylase (GTP)?";
 RL J. Biol. Chem. 266:17257-17260(1991).
 FT NON TER 1
 SQ SEQUENCE 8 AA; 819 MW; C3672DCAEDD04AEA CRC64;

Query Match 12.0%; Score 3; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALP 6
 DB 6 ALP 8

RESULT 47
 Q9R7H9 PRELIMINARY; PRT; 9 AA.
 ID Q9R7H9 PRELIMINARY; PRT; 9 AA.
 AC Q9R7H9; 2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE Lipoprotein (Fragment).
 GN NLDP.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98083063; PubMed=9422600;
 RA Martin K., Morlin G., Smith A., Nordsyke A., Eisenstark A., Golomb M.;
 RT "The tryptophanase gene cluster of Haemophilus influenzae type b:
 evidence for horizontal gene transfer.";
 RL J. Bacteriol. 180:1107-1118(1998).
 DR EMBL; AF003252; AAB9582.1; -.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1152 MW; 35A017673B4412D7 CRC64;

Query Match 12.0%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPR 7
 DB 6 LPR 8

RESULT 48
 Q14277 PRELIMINARY; PRT; 9 AA.
 ID Q14277 PRELIMINARY; PRT; 9 AA.
 AC Q14277; 1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
 DE RT protein short form (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94071887; PubMed=7902707;
 RA Ceccherini I., Bocciaardi R., Luo Y., Pasini B., Hofstra R.,
 RA Takahashi M., Romeo G.

RA Jenkins N.A., Harbers K.;
RT "Structure of the gene encoding the ubiquitin-conjugating enzyme
RL UbcM4, characterization of its promoter, and chromosomal location.",
RN Gene 224:109-116(1998).
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Mueller U., Grams A., Martinez-Noel G., Harbers K.,
RL Submitted (JUN-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF071557; AAD10128.1;
FT NON TER
SQ SEQUENCE 9 AA; 1063 MW; C90F97341415BDD CRC64;
Query Match 12.0%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
QY 2 MAA 4
DB 1 MAA 3
RESULT 53
Q90350 PRELIMINARY; PRT; 9 AA.
ID Q90350
AC Q90350; (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OC NCBI_TaxID=45255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SG3419;
RX MEDLINE=99266893; PubMed=10335862;
RA Wong S.B.J., Chan S.H., Ren E.C.,
RT "Diversity of GB virus C/hepatitis G virus isolates in Singapore:
RT predominance of group 2a and the Asian group 3 variant.",
RL J. Med. Virol. 58:145-153(1999).
DR EMBL; AF078065; AAC32371.1;
FT NON TER
SQ SEQUENCE 9 AA; 989 MW; D95CA5A5BEB9CDDD CRC64;
Query Match 12.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
QY 2 MAA 4
DB 1 MAA 3
RESULT 54
Q9E1U7 PRELIMINARY; PRT; 9 AA.
ID Q9E1U7
AC Q9E1U7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-DEC-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2F-8;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.,
RT "Sequence variation of Hepatitis B virus promoter regions in

RT by protein kinase C.;
RL Arch. Biochem. Biophys. 288:538-542(1991).
RN NON TER
RP SEQUENCE 9 AA; 1018 MW; 8C901B10533735A5 CRC64;
Query Match 12.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
QY 19 SLK 21
DB 3 SLK 5
RESULT 51
Q988J8 PRELIMINARY; PRT; 9 AA.
ID Q988J8
AC Q988J8;
DT 1-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ORYZATENSIN-BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.,
RT "Isolation and characterization of oryzatensin: a novel bioactive
RT peptide with ileum-contracting and immunomodulating activities derived
RT from rice albumin.",
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Biochem. Mol. Biol. Int. 33:1151-1158(1994).
FT NON TER
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;
Query Match 12.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
QY 5 LPR 7
DB 7 LPR 9
RESULT 52
Q98889 PRELIMINARY; PRT; 9 AA.
ID Q98889
AC Q98889;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ubiquitin-conjugating enzyme UBCM4 (Fragment).
GN UBCM4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=97057256; PubMed=8901595;
RA Harbers K., Muller U., Grams A., Li E., Jaenisch R., Franz T.,
RT "Provirus integration into a gene encoding a ubiquitin-conjugating
RT enzyme results in a placental defect and embryonic lethality.",
RL Proc. Natl. Acad. Sci. U.S.A. 93:12412-12417(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=99132641;
RA Mller U., Grams A., Martinez-Noel G., Copeland N.G., Gilbert D.J.,

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RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276526; AAG29993.1; -.
FT NON TER 9 9
SQ SEQUENCE 9 AA, 994 MW, CD0FDEBEA2D40DDD CRC64;

Query Match 12.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
Db 1 MAA 3

RESULT 55
Q9X533 PRELIMINARY; PRT; 10 AA.
ID Q9X533
AC Q9X533;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RL bacteria isolated from the fecal flora of primates.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RL gram-negative fecal bacteria of primates.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RX MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL; AF120964; AAD23783.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA, 1093 MW, 3F526335A5A7B58 CRC64;

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
Db 7 SLK 9

Search completed: December 19, 2002, 17:43:41
Job time : 29 secs

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Thu Dec 19 17:47:38 2002

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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:06 / Search time 34 Seconds
(without alignments)
97.978 Million cell updates/sec

Title: US-09-441-061-2
Perfect score: 25
Sequence: 1 GMAALPRLIAFTSEHSHSLKGA 25

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 320054

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database: A_Geneseq_101002.*
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3: /SID22/cgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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19: /SID22/cgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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21: /SID22/cgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/cgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/cgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
|------------|-------|-------------|----------------|--------------------|
| 1 | 25 | 100.0 | 25 16 AAR98667 | Human glutamic aci |
| 2 | 25 | 100.0 | 25 18 AAR18848 | 65 KD Glutamic aci |
| 3 | 16 | 64.0 | 20 16 AAR72279 | Glutamic acid deca |
| 4 | 16 | 64.0 | 20 21 AAY59552 | GAD65 fragment, pe |
| 5 | 14 | 56.0 | 20 16 AAR72278 | Glutamic acid deca |
| 6 | 14 | 56.0 | 20 21 AAY59578 | GAD65 fragment, pe |
| 7 | 9 | 36.0 | 20 21 AAY57065 | Glutamate decarbox |
| 8 | 8 | 32.0 | 24 21 AAB07785 | Glutamic acid deca |
| 9 | 6 | 24.0 | 19 18 AAW36759 | Thrombopoietin rec |
| 10 | 6 | 24.0 | 19 18 AAW09608 | Thrombopoietin rec |

| | | | | | | |
|----|---|------|----|----|----------|--------------------|
| 11 | 6 | 24.0 | 19 | 22 | AAU25978 | Human thrombopoiet |
| 12 | 5 | 20.0 | 8 | 16 | AAW21217 | Farnesyl synthetas |
| 13 | 5 | 20.0 | 8 | 22 | AAJ00161 | Hepatitis C virus |
| 14 | 5 | 20.0 | 8 | 22 | AAJ00801 | Hepatitis C virus |
| 15 | 5 | 20.0 | 8 | 22 | AAJ01077 | Hepatitis C virus |
| 16 | 5 | 20.0 | 8 | 22 | AAJ01728 | Hepatitis C virus |
| 17 | 5 | 20.0 | 8 | 22 | AAJ02447 | Hepatitis C virus |
| 18 | 5 | 20.0 | 8 | 22 | AAJ02598 | Hepatitis C virus |
| 19 | 5 | 20.0 | 8 | 22 | AAJ02836 | Hepatitis C virus |
| 20 | 5 | 20.0 | 8 | 22 | AAJ02983 | Hepatitis C virus |
| 21 | 5 | 20.0 | 9 | 18 | AAW43336 | Immunogenic HLA-A2 |
| 22 | 5 | 20.0 | 9 | 21 | AAJ73109 | Hepatitis C virus |
| 23 | 5 | 20.0 | 9 | 22 | AAJ00023 | Hepatitis C virus |
| 24 | 5 | 20.0 | 9 | 22 | AAJ00689 | Hepatitis C virus |
| 25 | 5 | 20.0 | 9 | 22 | AAJ01005 | Hepatitis C virus |
| 26 | 5 | 20.0 | 9 | 22 | AAJ01837 | Hepatitis C virus |
| 27 | 5 | 20.0 | 9 | 22 | AAJ02599 | Hepatitis C virus |
| 28 | 5 | 20.0 | 9 | 22 | AAJ02963 | Hepatitis C virus |
| 29 | 5 | 20.0 | 9 | 22 | AAJ03126 | Hepatitis C virus |
| 30 | 5 | 20.0 | 9 | 22 | AAJ03222 | Hepatitis C virus |
| 31 | 5 | 20.0 | 9 | 22 | AAJ03432 | Hepatitis C virus |
| 32 | 5 | 20.0 | 9 | 22 | AAJ03529 | Hepatitis C virus |
| 33 | 5 | 20.0 | 9 | 22 | AAJ03614 | Hepatitis C virus |
| 34 | 5 | 20.0 | 9 | 22 | AAJ03788 | Hepatitis C virus |
| 35 | 5 | 20.0 | 9 | 22 | AAJ03867 | Hepatitis C virus |
| 36 | 5 | 20.0 | 9 | 22 | AAJ03956 | Hepatitis C virus |
| 37 | 5 | 20.0 | 9 | 22 | AAJ03965 | Hepatitis C virus |
| 38 | 5 | 20.0 | 9 | 22 | AAJ04087 | Hepatitis C virus |
| 39 | 5 | 20.0 | 9 | 22 | AAJ76345 | Human secreted pro |
| 40 | 5 | 20.0 | 9 | 22 | AAJ59489 | Immunogenic peptid |
| 41 | 5 | 20.0 | 9 | 23 | AAU95868 | Peptide derived fr |
| 42 | 5 | 20.0 | 10 | 17 | AAW01985 | Human complementar |
| 43 | 5 | 20.0 | 10 | 22 | AAJ96799 | Hepatitis C virus |
| 44 | 5 | 20.0 | 10 | 22 | AAJ01931 | Hepatitis C virus |
| 45 | 5 | 20.0 | 10 | 22 | AAJ02783 | Hepatitis C virus |
| 46 | 5 | 20.0 | 11 | 16 | AAW21218 | Farnesyl synthetas |
| 47 | 5 | 20.0 | 11 | 22 | AAJ00088 | Hepatitis C virus |
| 48 | 5 | 20.0 | 11 | 22 | AAJ00671 | Hepatitis C virus |
| 49 | 5 | 20.0 | 11 | 22 | AAJ00826 | Hepatitis C virus |
| 50 | 5 | 20.0 | 11 | 22 | AAJ00842 | Hepatitis C virus |
| 51 | 5 | 20.0 | 11 | 22 | AAJ01943 | Hepatitis C virus |
| 52 | 5 | 20.0 | 11 | 22 | AAJ02021 | Hepatitis C virus |
| 53 | 5 | 20.0 | 11 | 22 | AAJ02097 | Hepatitis C virus |
| 54 | 5 | 20.0 | 11 | 22 | AAJ02448 | Hepatitis C virus |
| 55 | 5 | 20.0 | 11 | 22 | AAJ02600 | Hepatitis C virus |
| 56 | 5 | 20.0 | 11 | 22 | AAJ02837 | Hepatitis C virus |
| 57 | 5 | 20.0 | 11 | 22 | AAJ02922 | Hepatitis C virus |
| 58 | 5 | 20.0 | 12 | 15 | AAJ67053 | Neurotrophic Facto |
| 59 | 5 | 20.0 | 14 | 16 | AAJ67638 | Epitope of Non-A |
| 60 | 5 | 20.0 | 14 | 22 | AAJ00613 | Human protein frag |
| 61 | 5 | 20.0 | 14 | 22 | AAJ00614 | Human protein frag |
| 62 | 5 | 20.0 | 15 | 19 | AAW85435 | Helper T-cell clas |
| 63 | 5 | 20.0 | 15 | 19 | AAW85271 | Helper T-cell pept |
| 64 | 5 | 20.0 | 15 | 19 | AAW85282 | Helper T-cell pept |
| 65 | 5 | 20.0 | 15 | 21 | AAJ73095 | Hepatitis C virus |
| 66 | 5 | 20.0 | 15 | 22 | ABG27780 | Novel human diagno |
| 67 | 5 | 20.0 | 15 | 22 | AAJ03084 | Hepatitis C virus |
| 68 | 5 | 20.0 | 15 | 22 | AAJ03180 | Hepatitis C virus |
| 69 | 5 | 20.0 | 15 | 22 | AAJ03267 | Hepatitis C virus |
| 70 | 5 | 20.0 | 15 | 22 | AAJ03390 | Hepatitis C virus |
| 71 | 5 | 20.0 | 15 | 22 | AAJ03487 | Hepatitis C virus |
| 72 | 5 | 20.0 | 15 | 22 | AAJ03572 | Hepatitis C virus |
| 73 | 5 | 20.0 | 15 | 22 | AAJ03657 | Hepatitis C virus |
| 74 | 5 | 20.0 | 15 | 22 | AAJ04013 | Hepatitis C virus |
| 75 | 5 | 20.0 | 15 | 22 | AAJ04014 | Hepatitis C virus |

ALIGNMENTS

RESULT 1
AAR88667
ID AAR88667 standard; peptide; 25 AA.

PT dependent diabetes, also related nucleic acid, vectors,
PT antibodies, hybridoma(s) etc.
XX Example 11; Page 76; 100pp; English.
XX
CC AAQ86481 and AAQ86482 encode AAR71733 and AAR79105, rat and human
CC glutamic acid decarboxylase (GAD65) respectively, from which the GAD65
CC fragments described in AAR72261-R72298 were derived. These fragments
CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC and treat GAD-related autoimmune disorders, such as insulin
CC dependant diabetes mellitus or stiff man disease.
XX
XX SQ Sequence 20 AA;
Query Match 64.0%; Score 16; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 APTSEHSHFSLKKGAA 25
DB 1 APTSEHSHFSLKKGAA 16
|||||
RESULT 4
AAY59552
ID AAY59552 standard; peptide; 20 AA.
XX AC AAY59552;
XX
XX DT 03-APR-2000 (first entry)
XX
XX DE GAD65 fragment, peptide #19.
XX
XX KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
XX insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
XX therapy.
XX OS Homo sapiens.
XX
XX PN US5998366-A.
XX
XX PD 07-DEC-1999.
XX
XX PF 09-APR-1997; 97US-0827618.
XX
XX PR 07-JUN-1995; 95US-0485725.
XX
XX PR 21-SEP-1990; 90US-0586536.
XX
XX PR 18-JUN-1991; 91US-0718909.
XX
XX PA (REGC) UNIV CALIFORNIA.
XX
XX PI Tobin AJ, Kaufman DL, Erlander MG;
XX
XX DR WPI; 2000-095930/08.
XX
XX PT Ameliorating glutamic acid decarboxylase associated autoimmune
XX disorders such as insulin dependent diabetes mellitus and Stiff man
XX disease -
XX
XX PS Claim 1; Column 42; 61pp; English.
XX
CC This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and Stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.
XX

SQ Sequence 20 AA;
Query Match 64.0%; Score 16; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 APTSEHSHFSLKKGAA 25
DB 1 APTSEHSHFSLKKGAA 16
|||||
RESULT 5
AAR72278
ID AAR72278 standard; Peptide; 20 AA.
XX AC AAR72278;
XX
XX DT 13-NOV-1995 (first entry)
XX
XX DE Glutamic acid decarboxylase (GAD65) fragment.
XX
XX KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
XX insulin-dependant diabetes mellitus; stiff man disease.
XX OS Homo sapiens.
XX
XX PN WO9507992-A.
XX
XX PD 23-MAR-1995.
XX
XX PF 24-AUG-1994; 94WO-US09478.
XX
XX PR 17-SEP-1993; 93US-0123859.
XX
XX PA (REGC) UNIV CALIFORNIA.
XX
XX PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
XX
XX DR WPI; 1995-131360/17.
XX
XX PT New polypeptide fragments of glutamic acid decarboxylase - for
XX diagnosis and treatment of autoimmune disease, esp. insulin
XX dependent diabetes, also related nucleic acid, vectors,
XX antibodies, hybridoma(s) etc.
XX
XX PS Example 11; Page 76; 100pp; English.
XX
XX CC AAQ86481 and AAQ86482 encode AAR71733 and AAR79105, rat and human
XX glutamic acid decarboxylase (GAD65) respectively, from which the GAD65
XX fragments described in AAR72261-R72298 were derived. These fragments
XX can be used to detect autoantibodies against GAD, e.g. to diagnose
XX and treat GAD-related autoimmune disorders, such as insulin
XX dependant diabetes mellitus or stiff man disease.
XX
XX SQ Sequence 20 AA;
Query Match 56.0%; Score 14; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GWAALPRLIAPTSE 14
DB 7 GWAALPRLIAPTSE 20
|||||
RESULT 6
AAY59578
ID AAY59578 standard; peptide; 20 AA.
XX AC AAY59578;
XX
XX DT 03-APR-2000 (first entry)
XX

DE GAD65 fragment, peptide #18.
 XX GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
 KW therapy.
 XX Homo sapiens.
 XX US998366-A.
 XX 07-DEC-1999.
 XX 09-APR-1997; 97US-0827618.
 XX 07-JUN-1995; 95US-0485725.
 XX 21-SEP-1990; 90US-0586536.
 XX 18-JUN-1991; 91US-0716909.
 XX (REGC) UNIV CALIFORNIA.
 XX Robin AJ, Kaufman DL, Erlander MG;
 XX WPI; 2000-095930/08.
 XX Ameliorating glutamic acid decarboxylase associated autoimmune
 XX disorders such as insulin dependent diabetes mellitus and Stiff man
 XX disease -
 XX Example 11; Column 42; 61pp; English.
 XX This sequence represents a fragment of the glutamic acid decarboxylase 65
 XX (GAD65) protein. The invention relates to a method of ameliorating GAD
 XX associated autoimmune disorders by administering a GAD65 peptide to the
 XX patient. The method can be used for ameliorating GAD associated
 XX autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 XX and Stiff man disease. GAD65 can also be useful for screening drugs that
 XX alter GAD function, for generating monoclonal antibodies and in
 XX immunocassays. GAD65 is an effective diagnostic tool for predicting IDDM
 XX and the diagnosis is quite easy. It is also possible to obtain much
 XX larger quantities of polypeptide via recombinant techniques than are
 XX available from natural sources.
 XX Sequence 20 AA;
 Query Match 56.0%; Score 14; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GMAALPRIAFTSE 14
 DB 7 GMAALPRIAFTSE 20
 RESULT 7
 AAY57065
 ID AAY57065 standard; peptide; 20 AA.
 XX AAY57065;
 AC AAY57065;
 DT 28-FEB-2000 (first entry)
 XX Glutamate decarboxylase peptide GAD p18.
 DE Neglected target tissue antigen; NNTA; autoimmunity; autoimmune response;
 KW immunotherapeutic agent; insulin dependent diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
 KW uveoretinitis; inflammatory response.
 XX Homo sapiens.
 XX WO9956763-A1.
 XX 11-NOV-1999.

XX 07-MAY-1999; 99WO-US10250.
 XX 07-MAY-1998; 98US-0084636.
 XX (REGC) UNIV CALIFORNIA.
 XX Kaufman DL, Tian J, Olcott A;
 XX WPI; 2000-052905/04.
 XX Administration of neglected target tissue antigens to modulate immune
 XX responses -
 XX Disclosure; Page 23; 79pp; English.
 XX Amino acid sequences AAY57063-Y57091 are examples of neglected target
 XX tissue antigens NNTAs. NNTAs are antigens (whole antigens or fragments)
 XX not involved in autoimmunity. These peptides and proteins are used in
 XX the method of the invention which involves administering an NNTA as an
 XX antigen based immunotherapeutic agent, to a host afflicted with an
 XX autoimmune response associated with an autoimmune disease. The
 XX immunotherapeutic agent is used to treat autoimmune diseases such as
 XX insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
 XX thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal
 XX inflammatory immune responses. The NNTA induces regulatory tolerance by
 XX elicitation of regulatory T cells among T cells recognizing the NNTA but
 XX not participating in the immune response. The NNTA are capable of
 XX recognition by substantial populations of uncommitted T cells which can
 XX be primed, or biased, towards regulatory responses to provide effective
 XX treatment. The NNTA are effective in regulating undesirable immune
 XX responses even when target determinants used as agents promoting
 XX tolerance agents have failed to induce an effective regulatory T cell
 XX response. NNTAs as agents promoting tolerance are anticipated to be safer
 XX than use of target determinants.
 XX Sequence 20 AA;
 Query Match 36.0%; Score 9; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PRLIAFTSE 14
 DB 12 PRLIAFTSE 20
 RESULT 8
 AAB07785
 ID AAB07785 standard; peptide; 24 AA.
 XX AAB07785;
 AC AAB07785;
 DT 07-NOV-2000 (first entry)
 XX Glutamic acid decarboxylase-65 (GAD-65) analogue peptide.
 DE Glutamic acid decarboxylase-65; GAD-65; autoimmune disease;
 KW insulin-dependent diabetes mellitus; IDDM; stiff man syndrome;
 KW cellular autoimmune response; T-cell receptor; autoimmune antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Key
 FT Misc-difference 15
 FT /label= Thr, Glu
 XX EP1026238-A2.
 XX 09-AUG-2000.
 XX 17-JUN-1992; 2000EP-0102229.

CC The present sequence is a peptide which binds to thrombopoietin (TPO)
 CC receptor (TR). The compound can be used for treating patients suffering
 CC from haematological disorders and thrombocytopenia resulting from
 CC chemotherapy, radiation therapy or bone marrow transplantation. The
 CC peptide may also be used to maintain the proliferation and growth of
 CC TPO-dependent cell lines and for use in biological research, for
 CC detecting TPO receptors on living cells.

XX SQ Sequence 19 AA;
 Query Match 24.0%; Score 6; DB 18; Length 19;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 LKKGAA 25
 Db 10 LKKGAA 15
 |||||

RF 11
 AA 78
 ID AAU25978 standard; Peptide; 19 AA.
 XX AC AAU25978;
 DT 17-DEC-2001 (first entry)
 XX DE Human thrombopoietin receptor (TPO-R) activator peptide #164.

XX KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

XX OS Homo sapiens.
 XX PN US6251864-B1.
 XX PD 26-JUN-2001.
 XX PF 01-MAR-2000; 2000US-0516704.
 XX PR 07-JUN-1995; 95US-0478128.
 XX PR 07-JUN-1995; 95US-0485301.
 XX PR 07-JUN-1996; 96WO-US09623.
 XX PR 5-AUG-1996; 96US-0699027.
 XX PA (GLAXO) GLAXO GROUP LTD.
 XX PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz RJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB;
 PI Podduturi S, Yin Q;
 XX DR WPI; 2001-564142/63.

XX PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and haematological disorders, comprises contacting
 PT cells with peptides and peptide mimetics attached to hydrophilic
 PT polymers -
 XX PS Disclosure; Column 23; 128pp; English.

XX CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro

CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines.

XX SQ Sequence 19 AA;
 Query Match 24.0%; Score 6; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 LKKGAA 25
 Db 10 LKKGAA 15
 |||||

RESULT 12
 AAU21217
 ID AAU21217 standard; peptide; 8 AA.
 XX AC AAU21217;
 DT 29-JUL-1997 (first entry)
 XX DE Farnesyl synthetase derived signal oligopeptide #17.

XX KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rheus;
 KW gonadolibin precursor; plasminogen activator inhibitor 2; prorenin;
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
 KW apolipoprotein B; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
 KW Treponema pallidum membrana protein; TMPA; islet amyloid polypeptide;
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX OS Homo sapiens.
 XX PN WO9519568-A1.
 XX PD 20-JUL-1995.
 XX PF 12-JAN-1995; 95WO-US00575.
 XX PR 14-JAN-1994; 94US-0182248.
 XX PA (RATH/) RATH M.
 XX PI Rath M;
 XX DR WPI; 1995-263953/34.
 XX PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
 PT regions of max. hydrophilicity, used in modulating communication
 PT between protein(s)
 XX PS Claim 5; Page 25; 88pp; English.

XX CC The sequences given in AAU21201-560 represent hydrophilic signal oligo-
 CC peptides. These signal oligopeptides are localised on the surface
 CC of the protein and are represented by the hydrophilicity maxima of
 CC the protein. These peptides are enriched in charged amino acids
 CC arranged with neutral spacer amino acids. The specific signal
 CC character of these oligopeptides is determined by a characteristic
 CC combination of conformation and charge within the signal sequence.
 CC These oligopeptides may be used as vaccines in the treatment of

CC human disease, as competitive inhibitors to prevent or reduce the
 CC metabolic action or interaction of a selected protein by blocking
 CC its specific signal sequences, or as therapeutic agents to function
 CC as feedback regulators to reduce synthesis rate of a selected protein.
 CC These peptides may be modified by omitting one or more amino acids at
 CC the N- and/or C-terminal, by substituting one or more amino acids
 CC without consideration of charge and polarity, by substituting one or
 CC more amino acids with amino acid residues with similar charge and/or
 CC polarity, by omitting one or more amino acids or a combination of these.

XX SQ Sequence 8 AA;

Query Match 20.0%; Score 5; DB 16; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSLKK 22
 DB 2 FSLKK 6
 |||||

RESULT 13

AAJ00161
 ID AAJ00161 standard; Peptide; 8 AA.

XX AC AAJ00161;

XX DT 02-JUL-2001 (first entry)

XX DE Hepatitis C virus epitope #152.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PL Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus -
 XX PS Disclosure; Page 104; 214pp; English.

XX CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 8 AA;

Query Match 20.0%; Score 5; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
 DB 4 RLIAF 8
 |||||

RESULT 14

AAJ00801
 ID AAJ00801 standard; Peptide; 8 AA.

XX AC AAJ00801;

XX DT 02-JUL-2001 (first entry)

XX DE Hepatitis C virus epitope #792.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PL Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccines against hepatitis C virus -
 XX PS Disclosure; Page 120; 214pp; English.

XX CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 8 AA;

Query Match 20.0%; Score 5; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
 DB 1 RLIAF 5
 |||||

RESULT 15

AAJ01077
 ID AAJ01077 standard; Peptide; 8 AA.

XX AC AAJ01077;

XX DT 02-JUL-2001 (first entry)

XX DE Hepatitis C virus epitope #1069.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX

PA (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 127; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 8 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 8;
 XX Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 4 RLIAF 8

RESULT 16
 AAJ01728
 ID AAJ01728 standard; Peptide; 8 AA.
 XX AAJ01728;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #1719.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-A1.
 XX 29-MAR-2001.
 XX 9-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 XX (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 143; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 8 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 8;
 XX Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
 Db 4 RLIAF 8

RESULT 17
 AAJ02447
 ID AAJ02447 standard; Peptide; 8 AA.
 XX AAJ02447;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #2438.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-A1.
 XX 29-MAR-2001.
 XX 19-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 XX (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 160; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 8 AA;
 XX Query Match 20.0%; Score 5; DB 22; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 1 RLIAF 5

RESULT 18
 AAJ02598
 ID AAJ02598 standard; Peptide; 8 AA.
 XX AAJ02598;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #2589.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-A1.

XX Immunogen; binding motif; HLA-A2.1 allele; immunogenic peptide; cancer;
 KW glycoprotein; T cell activation; immune response; hepatitis C virus;
 KW human immunodeficiency virus type 1; HIV-1; vaccine; infection; antigen;
 KW HCV; HBV.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX WO9734621-A1.
 XX
 PD 25-SEP-1997.
 XX
 XX 21-MAR-1997; 97WO-US05348.
 XX
 PR 20-MAR-1997; 97US-0822382.
 PR 21-MAR-1996; 96US-0013980.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Grey HM, Sette A, Sidney J;
 XX
 DR WPI, 1997-479987/44.
 XX
 PT HLA-A2.1 binding peptide(s) - used in vaccines for the treatment and
 PT prevention of e.g. viral infection and cancer
 XX
 PS Claim 4; Page 29; 39pp; English.
 XX
 CC This sequence is an example of an immunogenic peptide having an HLA-A2.1
 CC binding motif, which is capable of inducing a T cell activation in T
 CC cells restricted by the A2.1 allele. This peptide is useful in eliciting
 CC an immune response against hepatitis C virus (HCV). The invention relates
 CC to a group of peptides having an HLA-A2.1 binding motif comprising 9 or
 CC 10 residues in which there is a first conserved residue at position 2
 CC selected from Leu, Met, Ile, Val, Ala and Thr and a second conserved
 CC residue at the C-terminus (position 9 or 10) selected from Val, Leu,
 CC Ile, Ala and Met. The immunogens are viral, e.g. human immunodeficiency
 CC virus type 1 (HIV-1), hepatitis B virus (HBV) and hepatitis C virus (HCV)
 CC or cancer antigens and are used in vaccines for the prevention and
 CC treatment of viral infection and cancer. The immunogens may be
 CC administered to the patient as a nucleic acid encoding the peptide
 CC (gene vaccine).
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 18; Length 9;
 Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 4 RLIAF 8
 RESULT 22
 AA73109
 ID AA73109 standard; Peptide; 9 AA.
 XX
 AC AA73109;
 XX
 XX 28-FEB-2000 (first entry)
 DT
 XX Hepatitis C virus (HCV)-derived MHC class I (CTL) epitope, #267.
 KW Chimeric; pan DR epitope; expression vector;
 KW promoter; major histocompatibility complex; MHC; targeting; peptide;
 KW epitope; antigen; presentation; class I; cytosolic pathway;
 KW endoplasmic reticulum; class II; extracellular antigen;
 KW endocytic pathway; helper T lymphocyte; HTL; universal epitope;
 KW cytotoxic T lymphocyte; CTL; immune response; immunogenicity; assay;
 KW vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV;
 KW hepatitis B; hepatitis C; bacterium; protozoan; tumour cell;

KW autoimmune disease; activation; antiviral; antimalarial;
 KW immunoprotective.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX WO9958658-A2.
 XX
 PD 18-NOV-1999.
 XX
 XX 13-MAY-1999; 99WO-US10646.
 PF
 PR 13-MAY-1998; 98US-0078904.
 PR 15-MAY-1998; 98US-0085751.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
 PI Chesnut RW;
 XX
 DR WPI; 2000-039103/03.
 XX
 PT Expression vectors encoding major histocompatibility targeting
 PT sequence, used as, e.g. tumor vaccines -
 XX
 PS Claim 11; Page 68; 130pp; English.
 XX
 CC Sequences AA73103-Y73145 represent hepatitis C virus (HCV)-derived MHC
 CC class I (CTL) epitopes which are claimed for use in the present
 CC invention. The invention relates to a novel expression vector comprising
 CC a promoter operably linked to a fusion gene encoding a major
 CC histocompatibility complex (MHC) targeting sequence, and two or more
 CC heterologous peptide epitopes. The MHC targeting sequence may be a
 CC class I targeting sequence, which directs an MHC class I epitope to
 CC a cytosolic pathway or to the endoplasmic reticulum, or an MHC class
 CC II targeting sequence, which directs extracellular antigens to
 CC enter the endocytic pathway to be processed into antigen peptides
 CC for presentation on MHC class II molecules. The heterologous
 CC epitopes may comprise either helper T lymphocyte (HTL) epitopes,
 CC or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL
 CC epitope such as a pan DR epitope (PADRE). The vectors are useful
 CC for stimulating an immune response in vivo, as well as for use in
 CC assaying the human immunogenicity of a human T cell peptide epitope in
 CC vivo in a non-human mammal. They provide a nucleic acid vaccine for
 CC enhancing immunity against infectious pathogens, such as viruses (e.g.,
 CC HIV, hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g.,
 CC Plasmodium falciparum, the cause of malaria) and also tumour cells and
 CC autoimmune diseases. Universal MHC class II epitopes are advantageously
 CC combined with other MHC class I and class II epitopes to increase the
 CC number of cells that are activated in response to a given antigen and
 CC provide a broader population coverage of MHC-reactive alleles.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 4 RLIAF 8
 RESULT 23
 AA700023
 ID AA700023 standard; Peptide; 9 AA.
 XX
 AC AA700023;
 XX
 XX 02-JUL-2001 (first entry)
 DT
 XX Hepatitis C virus epitope #14.
 DE
 XX

KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 OS WO200121189-A1.
 XX 29-MAR-2001.
 PD
 XX 19-JUL-2000; 2000WO-US19774.
 PF 19-JUL-1999; 99US-0357737.
 PR (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 DR
 XX A new composition useful as a vaccines against hepatitis C virus -
 PT Claim 1; Page 207; 214pp; English.
 XX
 PS The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8

RESULT 24
 AAJ00689
 ID AAJ00689 standard; Peptide; 9 AA.
 AC AAJ00689;
 XX 02-JUL-2001 (first entry)
 DT Hepatitis C virus epitope #680.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX antiviral.
 XX Hepatitis C virus.
 OS WO200121189-A1.
 XX 29-MAR-2001.
 PD
 XX 19-JUL-2000; 2000WO-US19774.
 PF 19-JUL-1999; 99US-0357737.
 PR (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 DR
 XX A new composition useful as a vaccines against hepatitis C virus -
 PT Claim 1; Page 207; 214pp; English.
 XX
 PS The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8

RESULT 25
 AAJ01005
 ID AAJ01005 standard; Peptide; 9 AA.
 AC AAJ01005;
 XX 02-JUL-2001 (first entry)
 DT Hepatitis C virus epitope #996.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX antiviral.
 XX Hepatitis C virus.
 OS WO200121189-A1.
 XX 29-MAR-2001.
 PD
 XX 19-JUL-2000; 2000WO-US19774.
 PF 19-JUL-1999; 99US-0357737.
 PR (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 DR
 XX A new composition useful as a vaccines against hepatitis C virus -
 PT Claim 1; Page 125; 214pp; English.
 XX
 PS The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 5 RLIAF 9

RESULT 26
 AAJ01837
 ID AAJ01837 standard; Peptide; 9 AA.

PS Disclosure; Page 117; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8

RESULT 25
 AAJ01005
 ID AAJ01005 standard; Peptide; 9 AA.
 AC AAJ01005;
 XX 02-JUL-2001 (first entry)
 DT Hepatitis C virus epitope #996.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX antiviral.
 XX Hepatitis C virus.
 OS WO200121189-A1.
 XX 29-MAR-2001.
 PD
 XX 19-JUL-2000; 2000WO-US19774.
 PF 19-JUL-1999; 99US-0357737.
 PR (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 DR
 XX A new composition useful as a vaccines against hepatitis C virus -
 PT Claim 1; Page 125; 214pp; English.
 XX
 PS The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 5 RLIAF 9

RESULT 26
 AAJ01837
 ID AAJ01837 standard; Peptide; 9 AA.


```

XX AAJ01837;
XX
XX 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #1828.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX
XX Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
XX 19-JUL-1999; 99US-0357737.
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Disclosure; Page 146; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 20.0%; Score 5; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 RLIAF 11
XX
XX DB 4 RLIAF 8
XX
XX RE. 27
XX AAJ02599
XX ID AAJ02599 standard; Peptide; 9 AA.
XX
XX AC AAJ02599;
XX
XX 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #2590.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX
XX Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
XX 19-JUL-1999; 99US-0357737.
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Disclosure; Page 146; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 20.0%; Score 5; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 RLIAF 11
XX
XX DB 4 RLIAF 8
XX

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PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Disclosure; Page 164; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 20.0%; Score 5; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 RLIAF 11
XX
XX DB 4 RLIAF 8
XX
XX RESULT 28
XX AAJ02963
XX ID AAJ02963 standard; Peptide; 9 AA.
XX
XX AC AAJ02963;
XX
XX 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #2954.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX
XX Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
XX 19-JUL-1999; 99US-0357737.
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Disclosure; Page 172; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 20.0%; Score 5; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 RLIAF 11
XX

```

Db 5 RLIAF 9

RESULT 29

AAJ03126
ID AAJ03126 standard; Peptide; 9 AA.

XX AC AAJ03126;

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #3117.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX XX 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccine against hepatitis C virus

XX PS Disclosure; Page 175; 214pp; English.

XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RLIAF 11

Db 3 RLIAF 7

RESULT 30

AAJ03222
ID AAJ03222 standard; Peptide; 9 AA.

XX AC AAJ03222;

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #3213.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX XX 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccine against hepatitis C virus

XX PS Disclosure; Page 176; 214pp; English.

XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RLIAF 11

Db 4 RLIAF 8

RESULT 31

AAJ03432
ID AAJ03432 standard; Peptide; 9 AA.

XX AC AAJ03432;

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #3423.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccine against hepatitis C virus

XX PS Disclosure; Page 178; 214pp; English.

XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.

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Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 3 RLIAF 7

RESULT 32
AAJ03529
ID AAJ03529 standard; Peptide; 9 AA.
XX AC AAJ03529;
XX DT 02-JUL-2001 (first entry)
XX DE hepatitis C virus epitope #3520.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-308046/32.
XX PT A new composition useful as a vaccines against hepatitis C virus -
XX PS Disclosure; Page 180; 214pp; English.
XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.
XX SQ Sequence 9 AA;
Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 4 RLIAF 8

RESULT 34
AAJ03788
ID AAJ03788 standard; Peptide; 9 AA.
XX AC AAJ03788;
XX DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #3779.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-308046/32.
XX PT A new composition useful as a vaccines against hepatitis C virus -
XX PS Disclosure; Page 187; 214pp; English.

us-09-441-061-2.rag

Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 3 RLIAF 7

RESULT 32
AAJ03529
ID AAJ03529 standard; Peptide; 9 AA.
XX AC AAJ03529;
XX DT 02-JUL-2001 (first entry)
XX DE hepatitis C virus epitope #3520.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-308046/32.
XX PT A new composition useful as a vaccines against hepatitis C virus -
XX PS Disclosure; Page 179; 214pp; English.
XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.
XX SQ Sequence 9 AA;
Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 4 RLIAF 8

RESULT 33
AAJ03614
ID AAJ03614 standard; Peptide; 9 AA.
XX AC AAJ03614;
XX DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #3605.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;

XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 CC
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8
 RESULT 35
 AAJ03867
 ID AAJ03867 standard; Peptide; 9 AA.
 XX
 AC AAJ03867;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #3858.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 PI WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 PS Example 2; Page 191; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 CC
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8
 RESULT 36
 AAJ03956
 ID AAJ03956 standard; Peptide; 9 AA.
 XX

AC AAJ03956;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #3947.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 PI WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 PS Example 2; Page 195; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 CC
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 5 RLIAF 9
 RESULT 37
 AAJ03965
 ID AAJ03965 standard; Peptide; 9 AA.
 XX
 AC AAJ03965;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #3956.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Example 3; Page 196; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 4 RLIAF 8
RESULT 38
AAJ04087
ID AAJ04087 standard; Peptide; 9 AA.
XX
XX AAJ04087;
XX
XX 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #4078.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX
XX Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
XX 19-JUL-1999; 99US-0357737.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Example 7; Page 203; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 4 RLIAF 8
RESULT 39
AAB76345
ID AAB76345 standard; Peptide; 9 AA.
XX
XX AAB76345;
XX
XX 10-APR-2001 (first entry)
XX
XX Hepatitis C virus immunogenic peptide..
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
XX HLA binding peptide; immune response; glycoprotein; cytostatic;
XX virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
XX human immunodeficiency virus; proteoacide; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
XX cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
XX renal carcinoma; cervical carcinoma; lymphoma; malaria;
XX condyloma acuminatum.
XX
XX Hepatitis C virus.
XX
XX WO200100225-A1.
XX
XX 04-JAN-2001.
XX
XX 28-JUN-2000; 2000WO-US17842.
XX
XX 29-JUN-1999; 99US-0141422.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S;
XX
XX WPI; 2001-112389/12.
XX
XX Composition comprising human leukocyte antigen binding peptide which
XX comprises isolated, prepared epitope useful for treating viral
XX infections such as acquired immunodeficiency syndrome, and cancer -
XX
XX Claim 1; Page 54; 58pp; English.
XX
XX The present invention describes a composition (I) which comprises at
XX least one human leukocyte antigen (HLA) binding peptide comprising an
XX isolated, prepared epitope comprising one of 347 8-11 residue amino acid
XX sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
XX virucide, hepatotropic, antiinflammatory, anti-HIV (human
XX immunodeficiency virus) and proteoacide activities, which can be used
XX in vaccine production and is an inducer of cytotoxic T-cell response.
XX (I) is useful for inducing a cytotoxic T cell response against a
XX preslected antigen in a patient expressing a specific major
XX histocompatibility complex (MHC) class I allele, by contacting cytotoxic
XX T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
XX treat and/or prevent viral infection and cancer such as prostate cancer,
XX hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
XX cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
XX carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
XX acuminatum.
XX
XX Sequence 9 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 5 RLIAF 9

RESULT 40
AAB59489
ID AAB59489 standard; Peptide; 9 AA.

XX AC AAB59489;
XX DT 22-MAR-2001 (first entry)
XX DE Human secreted protein #25.
XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; human; secreted protein.

XX OS Homo sapiens.
XX PN WO2000077173-A1.
XX PD 21-DEC-2000.

XX PF 01-JUN-2000; 2000WO-US14929.
XX PR 11-JUN-1999; 99US-0138573.
XX PR 07-JAN-2000; 2000US-0174851.

XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM, Komatsoulis GA;
XX DR WPI; 2001-071268/08.
XX DR N-PSDE; AAF23918.

XX PT Nucleic acids encoding 42 human secreted polypeptides, useful for
XX PT preventing, diagnosing and/or treating immune, hyperproliferative,
XX PT cardiovascular and neurological disorders or infectious diseases -
XX PS Claim 11; Page 430; 440pp; English.

XX SS Sequences AAB59465-B59506 represent the amino acid sequences of 42
XX CC human secreted proteins encoded by the genes AAF23894-P23935. The genes
XX CC and proteins are useful for preventing, ameliorating or treating medical
XX CC conditions, e.g. by protein or gene therapy. The genes are isolated from
XX CC a range of human tissues disclosed in the specification. The nucleic
XX CC acids, proteins, antibodies and (ant)agonists are useful in the
XX CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
XX CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
XX CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
XX CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX CC and parasitic infections.

XX SQ Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSE 14
DB 5 AFTSE 9

RESULT 41
AAU95868
ID AAU95868 standard; Peptide; 9 AA.
XX AC AAU95868;

XX DT 02-JUL-2002 (first entry)
XX DE Immunogenic peptide with (HLA)-A2.1 binding site #81.

XX KW HLA-A2.1 binding peptide; cytostatic; virucide; anti-HIV; hepatotropic;
XX KW human immunodeficiency virus; antiinflammatory; antibacterial; vaccine;
XX KW protozoacide; immunosuppressant; immunogenic peptide; T cell activation;
XX KW human leucocyte antigen binding site; cytotoxic T cell response;
XX KW viral infection; hepatitis; Epstein-Barr virus; papilloma virus;
XX KW human immunodeficiency virus; HIV; Kaposi sarcoma; lymphoma;
XX KW cytomegalovirus; tumour; prostate cancer; renal carcinoma; lymphoma;
XX KW prostate-specific antigen; p53; carcino-embryonal antigen;
XX KW melanoma antigen; Mycobacterium tuberculosis; protozoa;
XX KW trypanosome surface antigen; condyloma acuminatum.

XX OS Hepatitis C virus.

XX PN WO200220616-A1.

XX PD 14-MAR-2002.

XX PF 01-SEP-2000; 2000WO-US24102.

XX PR 01-SEP-2000; 2000WO-US24102.

XX PA (EPM-) EPIMUNE INC.

XX PI Grey HM, Sette A, Sidney J, Southwood S;
XX DR WPI; 2002-351766/38.

XX PT Immunogenic peptide with human leucocyte antigen-A2.1 binding site,
XX PT useful for treating e.g. viral infection or tumours -
XX PS Claim 1; Page 26; 35pp; English.

XX CC The invention describes a composition comprising an immunogenic peptide
XX CC having a human leucocyte antigen (HLA)-A2.1 binding site. The peptides
XX CC bind specifically to HLA-A2.1, to cause T cell activation and thus a
XX CC cytotoxic T cell response. The peptides and the nucleic acids that
XX CC encode them, are used, in vivo or ex vivo, for treatment of viral
XX CC infections (hepatitis B or C; Epstein-Barr; human immune deficiency;
XX CC Kaposi sarcoma; human papilloma; Lassa fever or cytomegalovirus);
XX CC tumours including prostate cancer, renal carcinoma and lymphoma (where
XX CC directed to prostate-specific antigen, p53, carcino-embryonal antigen,
XX CC Her2/neu or melanoma antigens); infection by Mycobacterium tuberculosis
XX CC or protozoa (directed to trypanosome surface antigen); and condyloma
XX CC acuminatum. The peptides are suitable for use in peptide-based
XX CC vaccines. This sequence represents an immunogenic peptide with the
XX CC human leucocyte antigen (HLA)-A2.1 binding site, described in the
XX CC invention.

XX SQ Sequence 9 AA;

Query Match 20.0%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 4 RLIAF 8

RESULT 42
AAW01985
ID AAW01985 standard; peptide; 10 AA.

XX AC AAW01985;

XX DT 26-SEP-1996 (first entry)

XX DE Peptide derived from hepatitis C virus NS4 protein.

```

XX Antigenic peptide; hepatitis C virus; HCV; non-A non-B;
KW non-structural protein 4; non-reactive; NS4;
KW
OS Hepatitis C virus.
XX
PN WO9604300-A1.
XX
XX WO9604300-A1.
XX
PD 15-FEB-1996.
XX
XX 28-JUL-1995; 95WO-US09599.
XX
XX 29-JUL-1994; 94US-0282758.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
XX
XX Fields HA, Khudyakov YE;
PI
XX PI; 1996-129330/13.
DF
XX Antigenic peptide(s) binding anti-hepatitis C virus antibodies -
PT useful for differential diagnosis of HCV in subjects
XX
XX Example; Page 29; 50pp; English.
XX
XX The present peptide, which was derived from the hepatitis C virus
CC (HCV) non-structural protein 4 (NS4), was prep'd. using Fmoc
CC chemistry. It was tested for reactivity against a panel of 32
CC anti-HCV positive sera, and was found to react with none of them.
XX
XX Sequence 10 AA;
SQ
Query Match 20.0%; Score 5; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 3 RLIAF 7
RESULT 43
AAG96799
ID AAG96799 standard; Peptide; 10 AA.
XX
AC AAG96799;
XX
XX 8-SEP-2001 (first entry)
DT
XX Human complementary peptide, SEQ ID NO: 2993.
XX
XX Human complementary peptide; ligand; drug discovery; drug design.
XX
XX Homo sapiens.
XX
XX WO200142277-A2.
XX
XX 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB04776.
XX
XX 13-DEC-1999; 99GB-0029464.
XX
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
XX
XX WPI; 2001-408419/43.
XX
XX A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT

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PT drug candidates or pro-drugs -
XX
XX Example 4; Page 472; 646pp; English.
XX
XX The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
XX Sequence 10 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ALPRL 8
DB 4 ALPRL 8
RESULT 44
AAJ01931
ID AAJ01931 standard; Peptide; 10 AA.
XX
AC AAJ01931;
XX
XX 02-JUL-2001 (first entry)
DT
XX Hepatitis C virus epitope #1922.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX
XX Hepatitis C virus.
OS
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
XX 19-JUL-1999; 99US-0357737.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R,
XX Baker DM, Celis E, Kubo RT, Grey HW;
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccine against hepatitis C virus -
XX
XX Disclosure; Page 148; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 10 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 6 RLIAF 10

```

RESULT 45
AAJ02783 standard; Peptide; 10 AA.
XX
XX AAJ02783;
XX
XX 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #2774.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX
XX antitiral.
XX
XX Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
XX 19-JUL-1999; 99US-0357737.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccine against hepatitis C virus -
XX
XX Disclosure; Page 168; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX
XX hepatitis C virus (HCV) epitope such as those given in AAJ0010-AAJ04121.
XX
XX These are derived from HCV HLA-binding motifs. They are useful in
XX
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX
XX
SQ Sequence 10 AA;
Query Match 20.0%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 3 RLIAF 7
RESULT 46
AAW21218 standard; peptide; 11 AA.
XX
XX AAJ02783;
XX
XX 29-JUL-1997 (first entry)
XX
XX Farnesyl synthetase derived signal oligopeptide #18.
XX
XX Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
XX
XX competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
XX
XX charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
XX
XX hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rheus;
XX
XX gonadoliben precursor; plasminogen activator inhibitor 2; prorenin;
XX
XX Alzheimer amyloid A4; corticotropin releasing factor binding protein;
XX
XX apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
XX
XX herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
XX
XX Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
XX
XX fibroblast WMP1; schistosoma elastase precursor; schistosomin;
XX
XX hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

OS Homo sapiens.
XX
XX WO9519568-A1.
XX
XX 20-JUL-1995.
XX
XX 12-JAN-1995; 95WO-US00575.
XX
XX 14-JAN-1994; 94US-0182248.
XX
XX (RATH/) RATH M.
XX
XX Rath M;
XX
XX WPI; 1995-263953/34.
XX
XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as
XX
XX regions of max. hydrophilicity, used in modulating communication
XX
XX between protein(s)
XX
XX Claim 5; Page 26; 8pp; English.
XX
XX The sequences given in AAJ21201-560 represent hydrophilic signal oligo-
XX
XX peptides. These signal oligopeptides are localised on the surface
XX
XX of the protein and are represented by the hydrophilicity maxima of
XX
XX the protein. These peptides are enriched in charged amino acids
XX
XX arranged with neutral spacer amino acids. The specific signal
XX
XX character of these oligopeptides is determined by a characteristic
XX
XX combination of conformation and charge within the signal sequence.
XX
XX These oligopeptides may be used as vaccines in the treatment of
XX
XX human disease, as competitive inhibitors to prevent or reduce the
XX
XX metabolic action or interaction of a selected protein by blocking
XX
XX its specific signal sequences, or as therapeutic agents to function
XX
XX as feedback regulators to reduce synthesis rate of a selected protein.
XX
XX These peptides may be modified by omitting one or more amino acids at
XX
XX the N- and/or C-terminal, by substituting one or more amino acids
XX
XX without consideration of charge and polarity, by substituting one or
XX
XX more amino acids with amino acid residues with similar charge and/or
XX
XX polarity, by omitting one or more amino acids or a combination of these.
XX
XX
XX
SQ Sequence 11 AA;
Query Match 20.0%; Score 5; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 FSLKK 22
DB 7 FSLKK 11
RESULT 47
AAJ00088 standard; Peptide; 11 AA.
XX
XX AAJ00088;
XX
XX 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #79.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX
XX antitiral.
XX
XX Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
XX 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX DR WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 103; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 11 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 PS Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 7 RLIAF 11
 RESULT 48
 AAJ00671
 ID AAJ00671 standard; Peptide; 11 AA.
 AC AAJ00671;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #662.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-Al.
 XX 29-MAR-2001.
 XX 9-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 XX (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 117; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 11 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 PS Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 7 RLIAF 11
 RESULT 49
 AAJ00826
 ID AAJ00826 standard; Peptide; 11 AA.
 AC AAJ00826;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #817.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-Al.
 XX 29-MAR-2001.
 XX 19-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 XX (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 121; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 11 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 PS Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8
 RESULT 50
 AAJ00842
 ID AAJ00842 standard; Peptide; 11 AA.
 AC AAJ00842;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #833.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX Query Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 6 RLIAF 10
 RESULT 49
 AAJ00826
 ID AAJ00826 standard; Peptide; 11 AA.
 AC AAJ00826;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #817.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-Al.
 XX 29-MAR-2001.
 XX 19-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 XX (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 121; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 11 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 PS Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8
 RESULT 50
 AAJ00842
 ID AAJ00842 standard; Peptide; 11 AA.
 AC AAJ00842;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #833.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX Query Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;

PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX PF
XX 19-JUL-1999; 99US-0357737.
XX PR
XX (EPIM-) EPIMMUNE INC.
XX PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HW;
XX PI
XX WPI; 2001-308046/32.
XX DR
XX A new composition useful as a vaccines against hepatitis C virus
XX PT
XX Disclosure; Page 122; 214pp; English.
XX PS
XX The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.
XX CC
XX SQ Sequence 11 AA;
Query Match 20.0%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 7 RLIAF 11
RESULT 51
AAJ01943
ID AAJ01943 standard; Peptide; 11 AA.
XX
XX AC AAJ01943;
XX
XX DT 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #1934.
XX DE
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.
XX OS
XX Hepatitis C virus.
XX OS
XX WO200121189-A1.
XX PN
XX PD 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX PF
XX 19-JUL-1999; 99US-0357737.
XX PR
XX (EPIM-) EPIMMUNE INC.
XX PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HW;
XX PI
XX WPI; 2001-308046/32.
XX DR
XX A new composition useful as a vaccines against hepatitis C virus
XX PT
XX Disclosure; Page 148; 214pp; English.
XX PS
XX The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.
XX CC

CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
XX SQ Sequence 11 AA;
Query Match 20.0%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 7 RLIAF 11
RESULT 52
AAJ02021
ID AAJ02021 standard; Peptide; 11 AA.
XX
XX AC AAJ02021;
XX
XX DT 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #2012.
XX DE
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.
XX OS
XX Hepatitis C virus.
XX OS
XX WO200121189-A1.
XX PN
XX PD 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX PF
XX 19-JUL-1999; 99US-0357737.
XX PR
XX (EPIM-) EPIMMUNE INC.
XX PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HW;
XX PI
XX WPI; 2001-308046/32.
XX DR
XX A new composition useful as a vaccines against hepatitis C virus
XX PT
XX Disclosure; Page 150; 214pp; English.
XX PS
XX The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.
XX CC
XX SQ Sequence 11 AA;
Query Match 20.0%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 6 RLIAF 10
RESULT 53
AAJ02097
ID AAJ02097 standard; Peptide; 11 AA.
XX
XX AC AAJ02097;
XX
XX DT 02-JUL-2001 (first entry)
XX

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DE Hepatitis C virus epitope #2088.
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX Hepatitis C virus.
XX WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX A new composition useful as a vaccine against hepatitis C virus -
XX Disclosure; Page 152; 214pp; English.
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX Sequence 11 AA;
XX Query Match 20.0%; Score 5; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 1 RLIAF 5
RESULT 55
AAJ02600
ID AAJ02600 standard; Peptide; 11 AA.
XX AC AAJ02600;
XX DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #2591.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX A new composition useful as a vaccine against hepatitis C virus -
XX Disclosure; Page 164; 214pp; English.
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX Sequence 11 AA;
XX Query Match 20.0%; Score 5; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 4 RLIAF 8
Search completed: December 19, 2002, 17:43:06

DE Hepatitis C virus epitope #2088.
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX Hepatitis C virus.
XX WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX A new composition useful as a vaccine against hepatitis C virus -
XX Disclosure; Page 152; 214pp; English.
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX Sequence 11 AA;
XX Query Match 20.0%; Score 5; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 7 RLIAF 11
RESULT 54
AAJ02448
ID AAJ02448 standard; Peptide; 11 AA.
XX AC AAJ02448;
XX DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #2439.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX

us-09-441-061-2.rag

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Job time : 35 secs

Thu Dec 19 17:47:44 2002

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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:06 ; Search time 15 seconds
(without alignments)
160.224 Million cell updates/sec

Title: US-09-441-061-2
Perfect score: 25
Sequence: 1 GNAALPRLIAFTSEHSFLKKGAA 25

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0
Total number of hits satisfying chosen parameters: 4984

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database : PIR.73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|---------------------|
| 1 | 5 | 20.0 | 25 | H64710 | hypothetical prote |
| 2 | 4 | 16.0 | 8 | XGHU8U | urine glycopeptide |
| 3 | 4 | 16.0 | 10 | PC2171 | triacylglycerol li |
| 4 | 4 | 16.0 | 15 | PA0087 | cytochrome c2 - fu |
| 5 | 4 | 16.0 | 18 | B48408 | 21K high mobility |
| 6 | 4 | 16.0 | 18 | S58277 | insulin-like growt |
| 7 | 4 | 16.0 | 20 | I54283 | arylsulfatase A - |
| 8 | 4 | 16.0 | 22 | A20527 | prostaglandin-endo |
| 9 | 3 | 12.0 | 5 | JN0860 | peptidyl-dipeptida |
| 10 | 3 | 12.0 | 6 | C22565 | R-phycocerythrin be |
| 11 | 3 | 12.0 | 7 | I48105 | dihydrofolate redu |
| 12 | 3 | 12.0 | 7 | S66442 | glutathione S-tran |
| 13 | 3 | 12.0 | 8 | A23967 | leucopyrrokinin - M |
| 14 | 3 | 12.0 | 9 | A24244 | adipokinetic hormo |
| 15 | 3 | 12.0 | 9 | A44873 | caldesmon - rabbit |
| 16 | 3 | 12.0 | 9 | A26363 | cardioactive pepti |
| 17 | 3 | 12.0 | 9 | A61620 | locustamyotropin I |
| 18 | 3 | 12.0 | 9 | S39766 | cardioactive pepti |
| 19 | 3 | 12.0 | 9 | S27233 | cardioactive pepti |
| 20 | 3 | 12.0 | 9 | PT0225 | ig heavy chain CDR |
| 21 | 3 | 12.0 | 9 | A60427 | macrophage cytotox |
| 22 | 3 | 12.0 | 9 | S78762 | ribosomal protein |
| 23 | 3 | 12.0 | 9 | A33527 | fructose-2,6-bisph |
| 24 | 3 | 12.0 | 9 | S39767 | cardioactive pepti |
| 25 | 3 | 12.0 | 9 | PC7073 | ubiquinol-cytochro |
| 26 | 3 | 12.0 | 9 | S15594 | orf 1 rara 5'-regl |
| 27 | 3 | 12.0 | 10 | A40624 | angiotensin I - Ja |
| 28 | 3 | 12.0 | 10 | C45474 | thrombospondin 2 - |
| 29 | 3 | 12.0 | 10 | G60787 | sperm-activating p |

| | | | | | | |
|----|---|------|----|---|--------|---------------------|
| 30 | 3 | 12.0 | 10 | 2 | C60787 | sperm-activating p |
| 31 | 3 | 12.0 | 10 | 2 | E60787 | sperm-activating p |
| 32 | 3 | 12.0 | 10 | 2 | E60527 | sperm-activating p |
| 33 | 3 | 12.0 | 10 | 2 | E39572 | sperm-activating p |
| 34 | 3 | 12.0 | 10 | 2 | D60589 | sperm-activating p |
| 35 | 3 | 12.0 | 10 | 2 | C60588 | sperm-activating p |
| 36 | 3 | 12.0 | 10 | 2 | A60588 | erythrocyte membra |
| 37 | 3 | 12.0 | 10 | 2 | XGHU8U | nitrogenase (EC 1. |
| 38 | 3 | 12.0 | 10 | 2 | S70251 | polygalacturonase |
| 39 | 3 | 12.0 | 10 | 2 | C61440 | hemoglobin, extrac |
| 40 | 3 | 12.0 | 10 | 2 | D61440 | acetylcholinestera |
| 41 | 3 | 12.0 | 10 | 2 | S65728 | angiotensin precur |
| 42 | 3 | 12.0 | 10 | 2 | A24196 | probable trpEG lea |
| 43 | 3 | 12.0 | 10 | 2 | A30917 | probable antigen 5 |
| 44 | 3 | 12.0 | 11 | 1 | LFTWNE | wound-induced prote |
| 45 | 3 | 12.0 | 11 | 2 | E41476 | hypothetical prote |
| 46 | 3 | 12.0 | 11 | 2 | S17775 | locustamyotropin - |
| 47 | 3 | 12.0 | 11 | 4 | S52252 | t-complex polypept |
| 48 | 3 | 12.0 | 12 | 1 | A43975 | malate dehydrogena |
| 49 | 3 | 12.0 | 12 | 2 | G49410 | polysialoglycoprot |
| 50 | 3 | 12.0 | 12 | 2 | PNO162 | T-cell receptor al |
| 51 | 3 | 12.0 | 12 | 2 | A28955 | insulin-like growt |
| 52 | 3 | 12.0 | 12 | 2 | PHL190 | ig gamma-2b chain |
| 53 | 3 | 12.0 | 12 | 2 | A60528 | T-cell receptor be |
| 54 | 3 | 12.0 | 12 | 2 | C30503 | lebetin 1 isoform |
| 55 | 3 | 12.0 | 12 | 2 | PH1481 | alpha-conotoxin GI |
| 56 | 3 | 12.0 | 12 | 2 | S71380 | glutathione peroxi |
| 57 | 3 | 12.0 | 13 | 1 | NTKN2G | ribosomal protein |
| 58 | 3 | 12.0 | 13 | 2 | A38929 | locustamyotropin I |
| 59 | 3 | 12.0 | 13 | 2 | S20578 | hypothetical prote |
| 60 | 3 | 12.0 | 13 | 2 | B61620 | polysialoglycoprot |
| 61 | 3 | 12.0 | 13 | 2 | S09395 | hemolytic protein |
| 62 | 3 | 12.0 | 13 | 2 | B28955 | ig heavy chain CRD |
| 63 | 3 | 12.0 | 13 | 2 | S09019 | conceptus protein |
| 64 | 3 | 12.0 | 13 | 2 | PT0290 | unidentified QM002 |
| 65 | 3 | 12.0 | 13 | 2 | B61233 | H+-transporting tw |
| 66 | 3 | 12.0 | 13 | 2 | PN0048 | mastoparan - yello |
| 67 | 3 | 12.0 | 13 | 2 | S01904 | trp operon leader |
| 68 | 3 | 12.0 | 14 | 1 | QMVAVV | somatostatin I - c |
| 69 | 3 | 12.0 | 14 | 1 | QMVHVM | somatostatin - spo |
| 70 | 3 | 12.0 | 14 | 1 | LPEBWT | somatostatin I - E |
| 71 | 3 | 12.0 | 14 | 2 | C60414 | somatostatin I - s |
| 72 | 3 | 12.0 | 14 | 2 | B60842 | |
| 73 | 3 | 12.0 | 14 | 2 | A60622 | |
| 74 | 3 | 12.0 | 14 | 2 | A60840 | |
| 75 | 3 | 12.0 | 14 | 2 | S00172 | |

ALIGNMENTS

RESULT 1

H64710 Hypothetical protein HP1528 - Helicobacter pylori (strain 26695)

CiSpecies: Helicobacter pylori

CiDate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

CiAccession: H64710

R.Tomb, J.P.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, J.D.; Kelley, J.M.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; PMID:97394467; PMID:9252185

A:Accession: H64710

A>Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-25 <POM>

A:Cross-references: GB:AE000651; GB:AE000511; NID:92314708; PIDN:ARD08577.1; PID:9231471

Query Match 20.0%; Score 5; DB 2; Length 25;
Best Local Similarity 100.0%; Pred.No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match      16.0%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 21 KKGA 24
    |||
Db 6 KKGA 9

RESULT 5
B48408
C:Species: Salmo salar (Atlantic salmon)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 07-Feb-1997
C:Accession: B48408
R:Waters, S.; Khamis, M.; Von Der Decken, A.
Cell. Mol. Biol. 38, 783-789, 1992
A:Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classification
A:Reference number: A48408
A:Accession: B48408
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <WAT>
C:Keywords: liver

Query Match      16.0%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGAA 25
    |||
Db 4 KGAA 7

RESULT 6
S58277
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C:Accession: S58277
R:Smrzka, O.W.; Stoger, R.; Kurzbauer, R.; Fae, I.; Fischer, G.P.; Barlow, D.P.
submitted to the EMBL Data Library, January 1995
A:Description: Conservation of a methylation imprint and a putative imprinting box at
A:Reference number: S58277
A:Accession: S58277
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <SMR>
A:Cross-references: EMBL:X83702; NID:929644; PIDN:CAA58675.1; PID:9929645
C:Keywords: growth factor receptor

Query Match      16.0%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 AALP 6
    |||
Db 9 AALP 12

RESULT 7
I54283
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I54283
R:Regis, S.; Carrozzo, R.; Filocamo, M.; Serra, G.; Mastropasolo, C.; Gatti, R.
Hum. Genet. 96, 233-235, 1995
A:Title: An An-deletion causing a frameshift in the arylsulphatase A gene of a late inf
A:Reference number: I54283
A:Accession: I54283
A:Status: preliminary; translated from GB/EMBL/DDBJ

Query Match      16.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 AALP 6
    |||
Db 3 AALP 6

RESULT 4
PA0087
C:Species: Fusarium sporotrichioides (fragment)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0087
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JTPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0087
A:Accession: PA0087
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: electron transfer; heme; photosynthesis

Query Match      16.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 EHSB 17
    |||
Db 2 EHSB 5

RESULT 3
PC2171
C:Species: Rhizopus niveus
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C:Accession: PC2171
R:Kohno, M.; Kugimiyu, W.; Hashimoto, Y.; Morita, Y.
Biochim. Biophys. Acta 1187, 1007-1012, 1994
A:Title: Purification, characterization, and crystallization of two types of lipase from
A:Reference number: PC2171; MUID:94319059; PMID:7765029
A:Accession: PC2171
A:Molecule type: protein
A:Residues: 1-10 <KOH>
C:Comment: This enzyme catalyzes the hydrolysis of the ester bonds.
C:Keywords: carboxylic ester hydrolase

Query Match      16.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 AALP 6
    |||
Db 3 AALP 6

RESULT 4
PA0087
C:Species: Fusarium sporotrichioides (fragment)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0087
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JTPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0087
A:Accession: PA0087
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: electron transfer; heme; photosynthesis

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us-09-441-061-2.rpr

A/Molecule type: DNA
 A/Residues: 1-20 <RES>
 A/Cross-references: GB:878735; NID:gl037139; PIDN:AA35013.1; PID:gl037140

Query Match 16.0%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPRL 8
 ||||
 Db 11 LPRL 14

RESULT 8

A20527
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) - sheep (fragment)
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 26-May-2000
 C/Accession: A20527
 R/Roth, G.J.; Machuga, E.T.; Ozols, J.
 Biochemistry 22; 4672-4675, 1983
 A/Title: Isolation and covalent structure of the aspirin-modified, active-site region of
 A/Reference number: A20527; MUID:84024608; PMID:6414516
 A/Accession: A20527
 A/Molecule type: protein
 A/Residues: 1-22 <ROT>
 A/Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 C/Keywords: oxidoreductase

Query Match 16.0%; Score 4; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSLK 21
 ||||
 Db 7 FSLK 10

RESULT 9

JN0860
 peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito
 C/Species: Sarda orientalis (striped bonito)
 C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C/Accession: JN0860
 R/Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57; 1743-1744, 1993
 A/Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
 A/Reference number: JN0859; MUID:94080036; PMID:7764272
 A/Accession: JN0860
 A/Molecule type: protein
 A/Residues: 1-5 <MAT>
 A/Experimental source: intestine
 C/Comment: The carboxyl-terminus is essential for the protein's expression of angiotensi
 C/Superfamily: bradykinin-potentiating peptide
 C/Keywords: angiotensin-converting enzyme inhibitor

Query Match 12.0%; Score 3; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALP 6
 ||||
 Db 1 ALP 3

RESULT 10

R23565
 R-phycoerythrin beta-1 chain - red alga (Gastrocloium coulteri) (fragment)
 C/Species: Gastrocloium coulteri
 C/Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C/Accession: R23565
 R/Klotz, A.V.; Glazer, A.N.
 J. Biol. Chem. 260; 4856-4863, 1985

A/Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A/Reference number: A22565; MUID:85182601; PMID:3886644
 A/Accession: C22565
 A/Molecule type: protein
 A/Residues: 1-6 <KLO>

Query Match 12.0%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
 ||||
 Db 1 MAA 3

RESULT 11

I48105
 dihydrofolate reductase - Chinese hamster (fragment)
 C/Species: Crictetus griseus (Chinese hamster)
 C/Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
 C/Accession: I48105
 R/Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
 Biochemistry 25; 6228-6236, 1986
 A/Title: Nucleotide sequence and nuclelease hypersensitivity of the Chinese hamster dihydr
 A/Reference number: I48105; MUID:87076541; PMID:3024702
 A/Accession: I48105
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-7 <RES>
 A/Cross-references: GB:M14771; NID:gl191055; PIDN:AAA36975.1; PID:gl191056

Query Match 12.0%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIA 10
 ||||
 Db 5 LIA 7

RESULT 12

S66442
 glutathione S-transferase P - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C/Accession: S66442
 R/Nishihira, J.; Sakai, M.; Nishi, S.; Hatanaka, Y.
 Eur. J. Biochem. 232; 106-110, 1995
 A/Title: Identification of the electrophilic substrate-binding site of glutat
 A/Reference number: S66442; MUID:96048035; PMID:7556138
 A/Accession: S66442
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-7 <NIS>

Query Match 12.0%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALP 6
 ||||
 Db 1 ALP 3

RESULT 13

A23967
 leucopyrokinin - Madeira cockroach
 C/Species: Leucophaea maderae (Madeira cockroach)
 C/Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 11-Jul-1997
 C/Accession: A23967
 R/Nachman, R.J.; Holman, G.M.; Cook, B.J.
 Biochem. Biophys. Res. Commun. 137; 936-942, 1986
 A/Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: structu

A;Reference number: A23967; PMID:86269041; PMID:3015140

A;Accession: A23967

A;Molecule type: protein

A;Residues: 1-8 <NAC>

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PRL 8

Db 6 PRL 8

RESULT 14

A24244

N;A; innatic hormone - bollworm

C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)

C;Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997

C;Accession: A24244

R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway

Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio

A;Reference number: A24244; PMID:86186794; PMID:3964263

A;Accession: A24244

A;Molecule type: protein

A;Residues: 1-9 <VAP>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 11 FTS 13

Db 4 FTS 6

RESULT 15

A44873

ca; mon - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

C;Accession: A44873

R;Ikeda, M.; Hornick, T.

Arch. Biochem. Biophys. 288, 538-542, 1991

A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by prote

A;Reference number: A44873; PMID:91378498; PMID:1898046

A;Accession: A44873

A;Molecule type: protein

A;Residues: 1-9 <IKE>

A;Experimental source: skeletal myosin

A;Note: sequence extracted from NCBI backbone (NCBI:63199)

C;Superfamily: caldesmon

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 19 SLK 21

Db 3 SLK 5

RESULT 16

A26363

cardioactive peptide - green crab (fragment)

C;Species: Carcinus maenas (green crab, common shore crab)

C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993

C;Accession: A26363

R;Scangier, J.; Hilbich, C.; Beyreuther, K.; Keller, R.

Proc. Natl. Acad. Sci. U.S.A. 84, 575-579, 1987

A;Title: Unusual cardioactive peptide (CCAP) from pericardial organs of the shore crat

A;Reference number: A26363

A;Accession: A26363

A;Molecule type: protein

A;Residues: 1-9 <STA>

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 10 APT 12

Db 5 APT 7

RESULT 17

A61620

locustamyotropin III - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997

C;Accession: A61620

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.

Insect Biochem. Mol. Biol. 22, 447-452, 1992

A;Title: Isolation, identification and synthesis of locustamyotropin III and IV, two a

A;Reference number: A61620

A;Accession: A61620

A;Molecule type: protein

A;Residues: 1-9 <SCH>

C;Keywords: amidated carboxyl end; neuropeptide

F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PRL 8

Db 7 PRL 9

RESULT 18

S39766

cardioactive peptide CCAP - yellow mealworm

C;Species: Tenebrio molitor (yellow mealworm)

C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 07-May-1999

C;Accession: S39766

R;Furuya, K.; Liao, S.; Reynolds, S.E.; Ota, R.B.; Hackett, M.; Schooley, D.A.

Biol. Chem. Hoppe-Seyler 374, 1065-1074, 1993

A;Title: Isolation and identification of a cardioactive peptide from Tenebrio molitor

A;Reference number: S39766; PMID:94176032; PMID:8129851

A;Accession: S39766

A;Molecule type: protein

A;Residues: 1-9 <FUR>

C;Keywords: neuropeptide

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 10 APT 12

Db 5 APT 7

RESULT 19

S27233
cardioactive peptide CCAP - tobacco hornworm
C/Species: Manduca sexta (tobacco hornworm)
C/Date: 09-Jun-1994 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C/Accession: S27233
R/Cheng, C.C.; Loi, P.K.; Sylwester, A.W.; Lee, T.D.; Tublitz, N.J.
FEBS Lett. 313, 165-168, 1992
A/Title: Primary structure of a cardioactive neuropeptide from the tobacco hawkmoth, *Manduca sexta*
A/Reference number: S27233; MUID:93050243; PMID:1426284
A/Accession: S27233
A/Molecule type: protein
A/Residues: 1-9 <CHE>
C/Keywords: neuropeptide

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 10 APT 12
|||
Db 5 APT 7

RESULT 20
PT0225
Ig heavy chain CDR3 region (clone 1-103) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0225
R/Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J_H gene usage in the development of the B cell repertoire
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0225
A/Molecule type: DNA
A/Residues: 1-9 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GMA 3
|||
Db 5 GMA 7

RESULT 21
A60427
macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993
C/Accession: A60427
R/Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
A/Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducing factor
A/Reference number: A60427; MUID:91372335; PMID:1909970
A/Accession: A60427
A/Molecule type: protein
A/Residues: 1-9 <JON>
A/Note: the sequence from the text on page 706 is inconsistent with that from page 708
C/Keywords: cytokine

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 23 GAA 25
|||
Db 1 GAA 3

RESULT 22
S78762
ribosomal protein MRP-S12, mitochondrial - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C/Accession: S78762
R/Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A/Reference number: S78760
A/Accession: S78762
A/Molecule type: protein
A/Residues: 1-9 <GRA>
C/Keywords: mitochondrial

P1-9/Product: ribosomal protein MRP-S12 (fragment) #status experimental <MAT>

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PRL 8
|||
Db 7 PRL 9

RESULT 23
A33527
fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.46) - rat (fragment)
N/Alternate names: fructose-2,6-bisphosphatase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jun-1993
C/Accession: A33527
R/Kitamura, K.; Uyeda, K.; Hartman, P.C.; Kangawa, K.; Matsuo, H.
J. Biol. Chem. 264, 6344-6348, 1989
A/Title: Catalytic site of rat liver and bovine heart fructose-6-phosphate, 2-kinase:fructose-2,6-bisphosphate 2-phosphatase
A/Reference number: A33527; MUID:89197937; PMID:2539378
A/Accession: A33527
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <KIT>
C/Keywords: phosphoric monoester hydrolase

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 AAL 5
|||
Db 6 AAL 8

RESULT 24
S39767
cardioactive peptide CCAP - Spodoptera eridania
C/Species: Spodoptera eridania
C/Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
C/Accession: S39767
R/Furuya, K.; Liso, S.; Reynolds, S.E.; Ota, R.B.; Hackett, M.; Schoolley, D.A.
Biochem. Biophys. Res. Commun. 193, 1065-1074, 1993
A/Title: Isolation and identification of a cardioactive peptide from *Tenebrio molitor* an
A/Reference number: S39766; MUID:94176032; PMID:8129851
A/Accession: S39767
A/Molecule type: protein
A/Residues: 1-9 <FUR>
C/Keywords: neuropeptide

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 10 APT 12
|||
Db 5 APT 7

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 |||
 Db 8 FSL 10

RESULT 28

C45474
 thrombospondin 2 - bovine (fragment)
 N;Alternate names: corticotropin-induced secreted protein (CISP); thrombospondin homol
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 14-Aug-1998
 C;Accession: C45474
 R;Pallerin, S.; Lafeuillade, B.; Scherrer, N.; Gagnon, J.; Shi, D.L.; Chambaz, E.M.; F
 J. Biol. Chem. 268, 4304-4310, 1993
 A;Title: Corticotropin-induced secreted protein, an ACTH-induced protein secreted by a
 A;Reference number: A45474; MUID:93179438; PMID:8382699
 A;Accession: C45474
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <PEL>
 A;Experimental source: adrenocortical cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:125844)
 C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology;

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
 |||
 Db 8 SLK 10

RESULT 29

G60787
 sperm-activating peptide (Ser-3,5,7 speract) - sea urchin (Anthocidaris crassispina).
 C;Species: Anthocidaris crassispina
 C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
 C;Accession: G60787
 R;Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka,
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocent
 A;Reference number: A60787; MUID:88242184; PMID:3378407
 A;Accession: G60787
 A;Molecule type: protein
 A;Residues: 1-10 <SUZ>
 C;Comment: This oligopeptide from egg jelly is one of several from this species, all o
 at shows some, but not absolute, species restriction.
 C;Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 |||
 Db 2 FSL 4

RESULT 30

C60787
 sperm-activating peptide (Ser-3,10 speract) - sea urchin (Hemicentrotus pulcherrimus)
 C;Species: Hemicentrotus pulcherrimus
 C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
 C;Accession: C60787
 R;Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka,
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocent
 A;Reference number: A60787; MUID:88242184; PMID:3378407
 A;Accession: C60787
 A;Molecule type: protein

RESULT 25
 PC7073
 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Jun-2002
 C;Accession: PC7073
 R;Taughta, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
 Electrophoresis 21, 1853-1871, 2000
 A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t
 A;Reference number: PC7072
 A;Accession: PC7073
 A;Molecule type: protein
 A;Residues: 1-9 <TSU>
 C;Keywords: brain; core protein; oxidoreductase

Query Match 12.0%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
 |||
 Db 1 SLK 3

RESULT 26

S15594
 orf 1 rara 5'-region - human
 C;Species: Homo sapiens (man)
 C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
 C;Accession: S15594
 R;Brand, N.J.; Petkovich, M.; Chambon, P.
 Nucleic Acids Res. 18, 6799-6806, 1990
 A;Title: Characterization of a functional promoter for the human retinoic acid receptor-
 A;Reference number: S15594; MUID:91088249; PMID:2175878
 A;Accession: S15594
 A;Molecule type: DNA
 A;Residues: 1-9 <BRA>
 A;Cross-references: EMBL:X56057; NID:g35875
 A;Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARAL, release 111.0
 C;Comment: This sequence is not thought to be translated.
 C;Genetics:
 A;Gene: GDB:RARA
 A;Cross-references: GDB:120337; OMIM:180240
 A;Map position: 17q12-17q12

Query Match 12.0%; Score 3; DB 4; Length 9;
 Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
 |||
 Db 1 MAA 3

RESULT 27

A60624
 angiotensin I - Japanese quail
 C;Species: Coturnix coturnix japonica (Japanese quail)
 C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
 C;Accession: A60624
 R;Takei, Y.; Hasegawa, Y.
 Gen. Comp. Endocrinol. 79, 12-22, 1990
 A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of thes
 A;Reference number: A60624; MUID:90284684; PMID:2191893
 A;Accession: A60624
 A;Molecule type: protein
 A;Residues: 1-10 <TAK>
 C;Superfamily: antithrombin III
 C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;

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A:Residues: 1-10 <SUZ>
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||
 Db 2 FSL 4

RESULT 31
 E60787
 sperm-activating peptide (Ser-3,5,7, Asp-10 speract) - sea urchin (Hemicentrotus pulcherrimus)
 C:Species: Hemicentrotus pulcherrimus
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
 C:Accession: E60787

R;Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A>Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
 A:Reference number: A60787; PMID:88242184; PMID:3378407

A:Accession: E60787
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 18 FSL 20
 ||||
 Db 2 FSL 4

RESULT 32
 E60527
 sperm-activating peptide (Ser-3, Gly-5 SAP-I) - sea urchin (Tripneustes gratilla)
 N:Alternate names: speract homolog TG-7
 C:Species: Tripneustes gratilla
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: E60527; G39572
 R;Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, M.;
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A>Title: A halogenated amino acid-containing sperm activating peptide and its related
 otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.

A:Reference number: A60527
 A:Accession: E60527
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 A>Note: this peptide did not contain bromophenylalanine
 R;Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Shimonishi, Y.;
 Biochemistry 30, 6203-6209, 1991
 A>Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate
 A:Reference number: A39572; PMID:91283461; PMID:2059627

A:Accession: G39572
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 A>Note: this peptide contained bromophenylalanine
 C:Superfamily: unassigned animal peptides
 F;2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20

Db 2 FSL 4
 ||||

RESULT 33

E39572
 sperm-activating peptide TG-5 - sea urchin (Tripneustes gratilla)

N:Alternate names: speract homolog TG-5
 C:Species: Tripneustes gratilla
 C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000

C:Accession: E39572
 R;Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Shimonishi, Y.;
 Biochemistry 30, 6203-6209, 1991
 A>Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate
 A:Reference number: A39572; PMID:91283461; PMID:2059627

A:Accession: E39572
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 C:Superfamily: unassigned animal peptides
 C:Keywords: bromine
 F;2/Modified site: 2'-bromophenylalanine (Phe) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||
 Db 2 FSL 4

RESULT 34

D60589
 sperm-activating peptide (Ser-3,5 SAP-I) - Echinometra mathaei

C:Species: Echinometra mathaei
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: D60589

R;Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, M.;
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A>Title: A halogenated amino acid-containing sperm activating peptide and its related
 otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.

A:Reference number: A60527
 A:Accession: D60589
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 A>Note: an identical peptide was isolated from Echinometra mathaei type A and type B
 C:Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||
 Db 2 FSL 4

RESULT 35

C60588
 sperm-activating peptide (Ser-3, Gly-5 SAP-I) - sea urchin (Strongylocentrotus nudus)

N:Alternate names: speract homolog
 C:Species: Strongylocentrotus nudus
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C:Accession: C60588
 R;Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, M.;
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A>Title: A halogenated amino acid-containing sperm activating peptide and its related
 otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.

A:Reference number: A60527
 A:Accession: C60588
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 C:Superfamily: unassigned animal peptides

elons as part of the nif1/2 gene clusters
 A:Reference number: S70242; MUID:96296457; PMID:8709854
 A:Accession: S70251
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-10 <SCH>
 A:Cross-references: EMBL:U25160; NID:g1160347; PIDN:AAC43540.1; PID:g1160348
 A:Experimental source: ATCC 29413
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
 C:Genetics:
 A:Gene: nifH2
 C:Keywords: ATP; iron-sulfur protein; nitrogen fixation; oxidoreductase

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IAF 11
 ||||
 DB 8 IAF 10

RESULT 39
 C61440
 polygalacturonase (EC 3.2.1.15) II b - Aspergillus sp. (fragment)
 C:Species: Aspergillus sp.
 C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996
 C:Accession: C61440
 R:Stratillova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jornvall, H.
 J. Protein Chem. 12, 15-22, 1993
 A:Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and st
 A:Reference number: A61440; MUID:93151962; PMID:8427629
 A:Accession: C61440
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <STR>
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 ||||
 DB 4 APT 6

RESULT 40
 D61440
 polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
 C:Species: Aspergillus sp.
 C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996
 C:Accession: D61440
 R:Stratillova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jornvall, H.
 J. Protein Chem. 12, 15-22, 1993
 A:Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and st
 A:Reference number: A61440; MUID:93151962; PMID:8427629
 A:Accession: D61440
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <STR>
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTS 13
 ||||
 DB 5 FTS 7

RESULT 41

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us-09-441-061-2.tpr

855728 hemoglobin, extracellular, chain di - earthworm (Lumbricus terrestris) (fragment).
 C/Species: Lumbricus terrestris (common earthworm)
 C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C/Accession: S65728
 R/Pushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
 Biochim. Biophys. Acta 1292, 273-280, 1996
 A/Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
 A/Reference number: S65721, MUID:96176855, PMID:8597573
 A/Accession: S65728
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <FUS>

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
 Db 7 SLK 9

RESULT 42
 A24196 acetylcholinesterase (EC 3.1.1.7) - electric eel (fragment)
 C/Species: Electrophorus electricus (electric eel)
 C/Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 28-Apr-1993
 C/Accession: A24196
 R/Kieffer, B.; Goeldner, M.; Hirth, C.; Aebersold, R.; Chang, J.Y.
 FEBS Lett. 202, 91-96, 1986
 A/Title: Sequence determination of a peptide fragment from electric eel acetylcholinesterase
 A/Reference number: A24196
 A/Accession: A24196
 A/Molecule type: protein
 A/Residues: 1-10 <KIE>
 C/Keywords: carboxylic ester hydrolase

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
 Db 7 GAA 9

RESULT 43
 A90917 angiotensin precursor - chicken (fragment)
 C/Species: Gallus gallus (chicken)
 C/Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
 C/Accession: A90917, A01250
 R/Nakayama, T.; Nakajima, T.; Sokabe, H.
 Chem. Pharm. Bull. 21, 2085-2087, 1973
 A/Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
 A/Reference number: A90917, MUID:74127845, PMID:4361802
 A/Accession: A90917
 A/Molecule type: protein
 A/Residues: 1-10 <NAK>
 C/Keywords: blood pressure control; hormone; vasoconstrictor
 F1-10/Product: angiotensin I #status experimental <ANL>
 F1-8/Product: angiotensin II #status experimental <AN2>

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 Db 8 FSL 10

RESULT 44
 LFTWE
 probable trpEG leader peptide - Thermus aquaticus
 C/Species: Thermus aquaticus
 C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
 C/Accession: S03315
 R/Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
 Biochim. Biophys. Acta 950, 303-312, 1988
 A/Title: Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and
 A/Reference number: S03315, MUID:89000781, PMID:2844259
 A/Accession: S03315
 A/Molecule type: DNA
 A/Residues: 1-11 <SAT>
 A/Cross-references: EMBL:X07744; NID:948261; PIDN:CAA30565.1; PID:948262
 A/Note: the source is designated as Thermus thermophilus HB8
 C/Genetics:
 A/Gene: trpL
 C/Superfamily: probable trpEG leader peptide

Query Match 12.0%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALP 6
 Db 2 ALP 4

RESULT 45
 E41476
 probable antigen 5 - Mycobacterium leprae (fragment)
 C/Species: Mycobacterium leprae
 C/Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 18-Jun-1993
 C/Accession: E41476
 R/Hartskeerl, R.A.; van Rens, R.M.; Stabel, L.F.E.M.; de Wit, M.Y.L.; Klatser, P.R.
 Infect. Immun. 58, 2821-2827, 1990
 A/Title: Selection and characterization of recombinant clones that produce Mycobacterium
 A/Reference number: A41476; MUID:90354041; PMID:1696931
 A/Accession: E41476
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-11 <HAR>

Query Match 12.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPR 7
 Db 4 LPR 6

RESULT 46
 S19775
 wound-induced protein - tomato (fragment)
 C/Species: Lycopersicon esculentum (tomato)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
 C/Accession: S19775
 R/Parsons, B.L.
 submitted to the EMBL Data Library, May 1991
 A/Reference number: S19773
 A/Accession: S19775
 A/Molecule type: mRNA
 A/Residues: 1-11 <PAR>
 A/Cross-references: EMBL:X59884; NID:919323; PID:919324

Query Match 12.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 23
 Db 5 KKG 7

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```

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <ROM>
A;Experimental source: reticulocyte
C;Superfamily: molecular chaperone t-complex-type

Query Match      12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 8 LIA 10
DB 2 LIA 4

RESULT 50
PN0162
malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994
C;Accession: PN0162
R;Fukaya, N.; Chow, L.P.; Sugiura, Y.; Taigita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotri
A;Reference number: PN0160
A;Accession: PN0162
A;Molecule type: protein
A;Residues: 1-12 <FUK>
C;Keywords: oxidoreductase

Query Match      12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 23 GAA 25
DB 7 GAA 9

RESULT 51
A28955
polyalloglycoprotein repeating unit - whitespotted char
C;Species: Salvelinus leucomaenis pluvius (whitespotted char)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Dec-1993
C;Accession: A28955
R;Kitajima, K.; Sorimachi, H.; Inoue, S.; Inoue, Y.
Biochemistry 27, 7141-7145, 1988
A;Title: Comparative structures of the apopolysialoglycoproteins from unfertilized and
A;Reference number: A90537; MUID:89062454; PMID:3196707
A;Accession: A28955
A;Molecule type: protein
A;Residues: 1-12 <KIT>
C;Keywords: glycoprotein

Query Match      12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 12 TSE 14
DB 4 TSE 6

RESULT 52
PH1190
T-cell receptor alpha chain V region (CW3/10.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1190
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.;
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recept
A;Reference number: S26512; MUID:92364546; PMID:1380061

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <ROM>
A;Experimental source: reticulocyte
C;Superfamily: molecular chaperone t-complex-type

Query Match      12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 8 LIA 10
DB 2 LIA 4

RESULT 50
PN0162
malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994
C;Accession: PN0162
R;Fukaya, N.; Chow, L.P.; Sugiura, Y.; Taigita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotri
A;Reference number: PN0160
A;Accession: PN0162
A;Molecule type: protein
A;Residues: 1-12 <FUK>
C;Keywords: oxidoreductase

Query Match      12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 23 GAA 25
DB 7 GAA 9

RESULT 51
A28955
polyalloglycoprotein repeating unit - whitespotted char
C;Species: Salvelinus leucomaenis pluvius (whitespotted char)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Dec-1993
C;Accession: A28955
R;Kitajima, K.; Sorimachi, H.; Inoue, S.; Inoue, Y.
Biochemistry 27, 7141-7145, 1988
A;Title: Comparative structures of the apopolysialoglycoproteins from unfertilized and
A;Reference number: A90537; MUID:89062454; PMID:3196707
A;Accession: A28955
A;Molecule type: protein
A;Residues: 1-12 <KIT>
C;Keywords: glycoprotein

Query Match      12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 12 TSE 14
DB 4 TSE 6

RESULT 52
PH1190
T-cell receptor alpha chain V region (CW3/10.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1190
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.;
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recept
A;Reference number: S26512; MUID:92364546; PMID:1380061

```

US-09-441-061-2.rpr

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A/Accession: PH1481
 A/Molecule type: mRNA
 A/Residues: 1-12 <CAS>
 A/Experimental source: cytolytic T-lymphocyte
 A/Note: the authors translated the codon GGT for residue 2 as Ala and GCT for residue 3
 C/Superfamily: immunoglobulin homology
 C/Keywords: receptor; T-cell

Query Match 12.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
 |||
 Db 2 GAA 4

Search completed: December 19, 2002, 17:44:02
 Job time : 16 secs

A/Accession: PH190
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <CAS>

Query Match 12.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SEH 15
 |||
 Db 4 SEH 6

RESULT 53
 A60528
 insulin-like growth factor-binding protein, serum - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
 C/Accession: A60528
 R/Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Ethernan, T.D.
 Comp. Biochem. Physiol. B 92, 561-567, 1989
 A/Title: Purification of the serum acid-stable insulin-like growth factor binding protein
 A/Reference number: A60528; MUID:89209787; PMID:2468442
 A/Accession: A60528
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-12 <WAL>

Query Match 12.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGA 24
 |||
 Db 2 KGA 4

RESULT 54
 C30503
 Ig gamma-2b chain C region (F5.5.1) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Aug-1996
 C/Accession: C30503
 R/Gilmore, G.L.; Bard, J.A.; Birshstein, B.K.
 J. Immunol. 141, 1754-1761, 1988
 A/Title: DNA rearrangements affecting both variable and constant regions of Ig H chain
 A/Reference number: A30503; MUID:88315788; PMID:2842402
 A/Accession: C30503
 A/Molecule type: mRNA
 A/Residues: 1-12 <GIL>
 A/Experimental source: myeloma cell line
 C/Keywords: immunoglobulin

Query Match 12.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 |||
 Db 10 PRL 12

RESULT 55
 PH1481
 T-cell receptor beta chain (clone A24/PEG2) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C/Accession: PH1481
 R/Casanova, J.L.; Martinon, P.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
 J. Exp. Med. 177, 811-820, 1993
 A/Title: T cell receptor selection by and recognition of two class I major histocompatib
 A/Reference number: PH1430; MUID:93171821; PMID:8436911

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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:06 / Search time 14 Seconds
(without alignments)
52.541 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25

Sequence: 1 GMAALPRLIAFTSEHSHFLKGA 25

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size: 0
Total number of hits satisfying chosen parameters: 147762

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database: Issued Patents AA*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 16 | 64.0 | 20 | 2 | US-08-484-530-32 |
| 2 | 16 | 64.0 | 20 | 2 | US-08-827-618A-32 |
| 3 | 16 | 64.0 | 20 | 3 | US-08-483-952A-32 |
| 4 | 16 | 64.0 | 20 | 4 | US-08-476-501-32 |
| 5 | 14 | 56.0 | 20 | 2 | US-08-484-530-31 |
| 6 | 14 | 56.0 | 20 | 2 | US-08-827-618A-31 |
| 7 | 14 | 56.0 | 20 | 3 | US-08-483-952A-31 |
| 8 | 14 | 56.0 | 20 | 4 | US-08-476-501-31 |
| 9 | 8 | 32.0 | 8 | 6 | 5475086-14 |
| 10 | 8 | 32.0 | 24 | 1 | US-08-485-718-2 |
| 11 | 8 | 32.0 | 24 | 2 | US-08-484-530-2 |
| 12 | 8 | 32.0 | 24 | 2 | US-08-827-618A-2 |
| 13 | 8 | 32.0 | 24 | 3 | US-08-483-952A-2 |
| 14 | 8 | 32.0 | 24 | 4 | US-08-476-501-2 |
| 15 | 6 | 24.0 | 19 | 2 | US-08-764-640-164 |
| 16 | 6 | 24.0 | 19 | 3 | US-08-973-225-164 |
| 17 | 6 | 24.0 | 19 | 3 | US-09-244-298A-164 |
| 18 | 6 | 24.0 | 19 | 4 | US-09-516-704-164 |
| 19 | 6 | 24.0 | 19 | 4 | US-09-549-090-164 |
| 20 | 5 | 20.0 | 10 | 1 | US-08-282-758B-6 |
| 21 | 5 | 20.0 | 12 | 2 | US-08-934-222-46 |
| 22 | 5 | 20.0 | 12 | 2 | US-08-933-402-46 |
| 23 | 5 | 20.0 | 12 | 2 | US-09-207-621-46 |
| 24 | 5 | 20.0 | 12 | 2 | US-08-532-818-46 |
| 25 | 5 | 20.0 | 12 | 3 | US-09-231-757-46 |
| 26 | 5 | 20.0 | 12 | 3 | US-08-934-224-46 |
| 27 | 5 | 20.0 | 12 | 3 | US-08-933-843-46 |

ALIGNMENTS

RESULT 1
US-08-484-530-32
Sequence 32, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

| | | | | | | |
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| 28 | 5 | 20.0 | 12 | 4 | US-08-934-223-46 | Sequence 46, Appl |
| 29 | 5 | 20.0 | 12 | 4 | US-09-413-492-46 | Sequence 46, Appl |
| 30 | 5 | 20.0 | 15 | 4 | US-09-009-953-173 | Sequence 173, App |
| 31 | 5 | 20.0 | 15 | 4 | US-09-009-953-184 | Sequence 184, App |
| 32 | 5 | 20.0 | 15 | 4 | US-09-009-953-258 | Sequence 258, App |
| 33 | 5 | 20.0 | 18 | 4 | US-09-109-957-11 | Sequence 11, Appl |
| 34 | 5 | 20.0 | 20 | 1 | US-08-282-758B-2 | Sequence 2, Appl |
| 35 | 5 | 20.0 | 21 | 4 | US-09-143-124-22 | Sequence 22, Appl |
| 36 | 5 | 20.0 | 21 | 4 | US-09-009-953-206 | Sequence 206, App |
| 37 | 5 | 20.0 | 21 | 4 | US-09-556-605-70 | Sequence 70, Appl |
| 38 | 5 | 20.0 | 21 | 4 | US-09-556-605-73 | Sequence 73, Appl |
| 39 | 5 | 20.0 | 21 | 5 | PCT-US92-07865-2 | Sequence 2, Appl |
| 40 | 5 | 20.0 | 22 | 4 | US-08-146-028-58 | Sequence 58, Appl |
| 41 | 5 | 20.0 | 22 | 4 | US-08-723-425A-58 | Sequence 58, Appl |
| 42 | 5 | 20.0 | 22 | 4 | US-09-112-206-58 | Sequence 58, Appl |
| 43 | 5 | 20.0 | 23 | 6 | 5475086-9 | Patent No. 5475086 |
| 44 | 5 | 20.0 | 24 | 3 | US-08-592-500-36 | Sequence 36, Appl |
| 45 | 5 | 20.0 | 24 | 3 | US-08-195-006-35 | Sequence 36, Appl |
| 46 | 5 | 20.0 | 24 | 5 | PCT-US92-07865-3 | Sequence 3, Appl |
| 47 | 5 | 20.0 | 24 | 5 | PCT-US94-07644A-36 | Sequence 36, Appl |
| 48 | 5 | 20.0 | 25 | 2 | US-08-452-242-1 | Sequence 1, Appl |
| 49 | 5 | 20.0 | 25 | 2 | US-08-934-741A-23 | Sequence 23, Appl |
| 50 | 5 | 20.0 | 25 | 3 | US-08-453-176A-1 | Sequence 1, Appl |
| 51 | 5 | 20.0 | 25 | 3 | US-08-451-374-1 | Sequence 1, Appl |
| 52 | 5 | 20.0 | 25 | 4 | US-08-935-268A-1 | Sequence 1, Appl |
| 53 | 5 | 20.0 | 25 | 4 | US-08-452-229-1 | Sequence 6, Appl |
| 54 | 4 | 16.0 | 4 | 3 | US-08-785-247-6 | Sequence 2, Appl |
| 55 | 4 | 16.0 | 6 | 1 | US-08-484-192-2 | Sequence 2, Appl |
| 56 | 4 | 16.0 | 6 | 3 | US-08-798-394-2 | Sequence 2, Appl |
| 57 | 4 | 16.0 | 6 | 4 | US-09-215-775-2 | Sequence 2, Appl |
| 58 | 4 | 16.0 | 7 | 4 | US-09-370-644B-20 | Sequence 20, Appl |
| 59 | 4 | 16.0 | 8 | 4 | US-08-953-033-19 | Sequence 19, Appl |
| 60 | 4 | 16.0 | 8 | 4 | US-08-988-842-49 | Sequence 49, Appl |
| 61 | 4 | 16.0 | 9 | 1 | US-07-942-245-504 | Sequence 504, App |
| 62 | 4 | 16.0 | 9 | 2 | US-08-705-660-3 | Sequence 3, Appl |
| 63 | 4 | 16.0 | 9 | 2 | US-08-350-260A-479 | Sequence 479, App |
| 64 | 4 | 16.0 | 9 | 3 | US-08-989-045-3 | Sequence 3, Appl |
| 65 | 4 | 16.0 | 9 | 3 | US-08-471-546-1 | Sequence 1, Appl |
| 66 | 4 | 16.0 | 9 | 3 | US-08-159-339A-978 | Sequence 978, App |
| 67 | 4 | 16.0 | 9 | 3 | US-08-471-586-6 | Sequence 6, Appl |
| 68 | 4 | 16.0 | 9 | 4 | US-08-482-918-69 | Sequence 69, Appl |
| 69 | 4 | 16.0 | 9 | 4 | US-09-224-681-69 | Sequence 69, Appl |
| 70 | 4 | 16.0 | 9 | 4 | US-08-336-728A-69 | Sequence 69, Appl |
| 71 | 4 | 16.0 | 10 | 1 | US-08-166-195A-38 | Sequence 38, Appl |
| 72 | 4 | 16.0 | 10 | 1 | US-08-166-195A-39 | Sequence 39, Appl |
| 73 | 4 | 16.0 | 10 | 1 | US-08-166-195A-40 | Sequence 40, Appl |
| 74 | 4 | 16.0 | 10 | 1 | US-08-346-333-62 | Sequence 62, Appl |
| 75 | 4 | 16.0 | 10 | 2 | US-08-436-772-38 | Sequence 38, Appl |


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1  INFORMATION FOR SEQ ID NO: 32:
2  SEQUENCE CHARACTERISTICS:
3  LENGTH: 20 amino acids
4  TYPE: amino acid
5  STRANDEDNESS: single
6  TOPOLOGY: linear
7  MOLECULE TYPE: peptide
8  US-08-827-618A-32
9
10 Query Match 64.0%; Score 16; DB 2; Length 20;
11 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
12 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
13
14 QY 10 APTSEHSHFSLKKGAA 25
15 DB 1 APTSEHSHFSLKKGAA 16
16
17 RESULT 3
18 US-08-483-952A-32
19 Sequence 32, Application US/08483952A
20 Patent No. 6011139
21 GENERAL INFORMATION:
22 APPLICANT: Tobin, Allan J
23 APPLICANT: Erlander, Mark G
24 APPLICANT: Kaufman, Daniel L.
25 TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
26 NUMBER OF SEQUENCES: 60
27 CORRESPONDENCE ADDRESS:
28 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
29 STREET: Four Embarcadero Center, Suite 3400
30 CITY: San Francisco
31 STATE: CA
32 COUNTRY: US
33 ZIP: 94111-4187
34 COMPUTER READABLE FORM:
35 MEDIUM TYPE: Floppy disk
36 COMPUTER: IBM PC compatible
37 OPERATING SYSTEM: PC-DOS/MS-DOS
38 SOFTWARE: Patent in Release #1.0, Version #1.30
39 CURRENT APPLICATION DATA:
40 APPLICATION NUMBER: US/08/483,952A
41 FILING DATE: 07-JUN-1995
42 CLASSIFICATION: 536
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: US 08/123,859
45 FILING DATE: 17-SEP-1993
46 CLASSIFICATION: 536
47 PRIOR APPLICATION DATA:
48 APPLICATION NUMBER: US 07/716,909
49 FILING DATE: 18-JUN-1991
50 CLASSIFICATION: 536
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: US 07/586,536
53 FILING DATE: 21-SEP-1990
54 CLASSIFICATION: 536
55 ATTORNEY/AGENT INFORMATION:
56 NAME: Trecartin, Richard F.
57 REGISTRATION NUMBER: 31,801
58 REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
59 TELECOMMUNICATION INFORMATION:
60 TELEPHONE: 415-781-1989
61 TELEFAX: 415-398-3249
62 INFORMATION FOR SEQ ID NO: 32:
63 SEQUENCE CHARACTERISTICS:
64 LENGTH: 20 amino acids
65 TYPE: amino acid
66 STRANDEDNESS: single
67 TOPOLOGY: linear
68 MOLECULE TYPE: peptide
69 US-08-483-952A-32
70
71 Query Match 64.0%; Score 16; DB 2; Length 20;
72 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
73 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
74
75 QY 10 APTSEHSHFSLKKGAA 25
76 DB 1 APTSEHSHFSLKKGAA 16
77
78 RESULT 2
79 US-08-827-618A-32
80 Sequence 32, Application US/08827618A
81 Patent No. 5998366
82 GENERAL INFORMATION:
83 APPLICANT: Tobin, Allan J
84 APPLICANT: Erlander, Mark G
85 APPLICANT: Kaufman, Daniel L.
86 TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
87 NUMBER OF SEQUENCES: 60
88 CORRESPONDENCE ADDRESS:
89 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
90 STREET: Four Embarcadero Center, Suite 3400
91 CITY: San Francisco
92 STATE: CA
93 COUNTRY: US
94 ZIP: 94111-4187
95 COMPUTER READABLE FORM:
96 MEDIUM TYPE: Floppy disk
97 COMPUTER: IBM PC compatible
98 OPERATING SYSTEM: PC-DOS/MS-DOS
99 SOFTWARE: Patent in Release #1.0, Version #1.30
100 CURRENT APPLICATION DATA:
101 APPLICATION NUMBER: US/08/827,618A
102 FILING DATE: 09-APR-1997
103 CLASSIFICATION: 435
104 PRIOR APPLICATION DATA:
105 APPLICATION NUMBER: US 08/485,725
106 FILING DATE: 07-JUN-1995
107 PRIOR APPLICATION DATA:
108 APPLICATION NUMBER: US 07/716,909
109 FILING DATE: 18-JUN-1991
110 PRIOR APPLICATION DATA:
111 APPLICATION NUMBER: US 07/586,536
112 FILING DATE: 21-SEP-1990
113 ATTORNEY/AGENT INFORMATION:
114 NAME: Trecartin, Richard F.
115 REGISTRATION NUMBER: 31,801
116 REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
117 TELECOMMUNICATION INFORMATION:
118 TELEPHONE: 415-781-1989
119 TELEFAX: 415-398-3249
120

```

us-09-441-061-2.rai

Thu Dec 19 17:47:39 2002

Best Local Similarity 100.0%; Pred. No. 1.6e-09; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSEHSHFLKKGAA 25
Db 1 AFTSEHSHFLKKGAA 16

RESULT 4

US-08-476-501-32
Sequence 32, Application US/08476501
Patent No. 6455267
GENERAL INFORMATION:
APPLICANT: TOBIN, Allan J.
APPLICANT: ERLANDER, Mark G.
APPLICANT: KAUFMAN, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,501
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60780-10/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-501-32

Query Match 64.0%; Score 16; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSEHSHFLKKGAA 25
Db 1 AFTSEHSHFLKKGAA 16

RESULT 5

US-08-484-530-31
Sequence 31, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: Erlander, Mark G.
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Irecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-31

Query Match 56.0%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAPTSE 14
Db 7 GMAALPRLIAPTSE 20

RESULT 6

US-08-827-618A-31
Sequence 31, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: Erlander, Mark G.
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:

us-09-441-061-2.ral

Thu Dec 19 17:47:39 2002

NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/NTK
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-31

Query Match 56.0%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSE 14
DB 7 GMAALPRLIAFTSE 20

RESULT 8

US-08-476-501-31
Sequence 31, Application US/08476501
Patent No. 645267
GENERAL INFORMATION:
APPLICANT: TOBIN, Allan J.
APPLICANT: ERLANDER, Mark G.
APPLICANT: KAUFMAN, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,501
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60780-10/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-501-31

Query Match 56.0%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSE 14
DB 7 GMAALPRLIAFTSE 20

RESULT 9

5475086-14
Patent No. 5475086
APPLICANT: TOBIN, ALLAN J.; ERLANDER, MARK G.; KAUFMAN, DANIEL L.; CLARE-SALZLER, MICHAEL J.
TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
NUMBER OF SEQUENCES: 14

NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/NTK
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-31

Query Match 56.0%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSE 14
DB 7 GMAALPRLIAFTSE 20

RESULT 7

US-08-483-952A-31
Sequence 31, Application US/08483952A
Patent No. 601139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: ERLANDER, Mark G.
APPLICANT: KAUFMAN, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/NTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid

US-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/135,849
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 716,909
; FILING DATE: 18-JUN-1991
; APPLICATION NUMBER: 586,536
; FILING DATE: 21-SEP-1990
; SEQ ID NO:14:
; LENGTH: 8
5475086-14

Query Match          32.0%; Score 8; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GMAALPRL 8
Db 1 GMAALPRL 8

RESULT 10
US-08-485-718-2
; Sequence 2, Application US/08485718
; Patent No. 5705626
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,718
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A60780-6/BIR
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-718-2

Query Match          32.0%; Score 8; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GMAALPRL 8
Db 17 GMAALPRL 24

RESULT 11
US-08-484-530-2
; Sequence 2, Application US/08484530
; Patent No. 5846740
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,530
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard P.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-530-2

Query Match          32.0%; Score 8; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GMAALPRL 8
Db 17 GMAALPRL 24

RESULT 12
US-08-827-618A-2
; Sequence 2, Application US/08827618A
; Patent No. 5998366
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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us-09-441-061-2.rai

Thu Dec 19 17:47:39 2002

FILING DATE: 21-SEP-1990
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-483-952A-2

Query Match 32.0%; Score 8; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels

Qy 1 GMAALPRL 8
|||
Dh 17 GMAALPRL 24
|||

RESULT 14
US-08-476-501-2
; Sequence 2, Application US/08476501
; Patent No. 6455267
; GENERAL INFORMATION:
; APPLICANT: TOBIN, Allan J.
; APPLICANT: ERLANDER, Mark G.
; APPLICANT: KAUFMAN, Daniel L.
; APPLICANT: KAUFMAN, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco

Query Match 32.0%; Score 8; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels

APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RPT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
FORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
UNP-08-827-618A-2

Query Match 32.0%; Score 8; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels

QY 1 GMAALPRL 8
|||
Dh 17 GMAALPRL 24

RESULT 13
US-08-483-952A-2
Sequence 2, Application US/08483952A
Patent No. 601139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
---CORRESPONDENCE ADDRESSES:
ADDRESSES: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/483,952A
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/586,536

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QY 1 GMAALPRL 8
 Db 17 GMAALPRL 24

RESULT 15
 US-08-764-640-164
 ; Sequence 164, Application US/08764640
 ; Patent No. 5869451
 ; Patent No. 5869451 5837683

GENERAL INFORMATION:
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Barrett, Ronald W.
 ; APPLICANT: Cwiria, Steven E.
 ; APPLICANT: Gates, Christian
 ; APPLICANT: Schatz, Peter J.
 ; APPLICANT: Balasubramanian, Palaniappan
 ; APPLICANT: Wagstrom, Christopher R.
 ; APPLICANT: Hendren, Richard W.
 ; APPLICANT: Deprince, Randolph B.
 ; APPLICANT: Poddaturi, Surekha
 ; APPLICANT: Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 RECEPTOR
 NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/764,640
 FILING DATE: 11-DEC-1996
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Hrubic, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3281
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 164:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: peptide
 MOLECULE TYPE: peptide

US-08-764-640-164
 Query Match 24.0%; Score 6; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25
 Db 10 LKKGAA 15

RESULT 16
 US-08-973-225-164
 ; Sequence 164, Application US/08973225A
 ; Patent No. 6083913
 ; GENERAL INFORMATION:
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Barrett, Ronald W.
 ; APPLICANT: Cwiria, Steven E.

Duffin, David J.
 Gates, Christian
 Haselden, Sherril S.
 Mattheakis, Larry C.
 Schatz, Peter J.
 Wagstrom, Christopher R.
 Wrighton, Nicholas C.
 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/973,225A
 FILING DATE: 04-DEC-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Hrubic, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3065USW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 164:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 164:
 US-08-973-225-164

Query Match 24.0%; Score 6; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25
 Db 10 LKKGAA 15

RESULT 17
 US-09-244-298A-164
 ; Sequence 164, Application US/09244298A
 ; Patent No. 6121238
 ; GENERAL INFORMATION:
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Barrett, Ronald W.
 ; APPLICANT: Cwiria, Steven E.
 ; APPLICANT: Gates, Christian
 ; APPLICANT: Schatz, Peter J.
 ; APPLICANT: Balasubramanian, Palaniappan
 ; APPLICANT: Wagstrom, Christopher R.
 ; APPLICANT: Hendren, Richard W.
 ; APPLICANT: Deprince, Randolph B.
 ; APPLICANT: Poddaturi, Surekha
 ; APPLICANT: Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 RECEPTOR
 NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park

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STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-516-704-164

Query Match 24.0%; Score 6; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25
DB 10 LKKGAA 15
|||||

RESULT 18
US-09-516-704-164
; Sequence 164, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Gates, Christian
; Schatz, Peter J.
; Balasubramanian, Palaniappan
; Wagstrom, Christopher R.
; Hendren, Richard W.
; Deprince, Randolph B.
; Poduturi, Surekha
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/516,704
; FILING DATE: 01-Mar-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-549-090-164

Query Match 24.0%; Score 6; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25
DB 10 LKKGAA 15
|||||

RESULT 19
US-09-549-090-164
; Sequence 164, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,090
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-549-090-164

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us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

US-09-207-621-46

Query Match 20.0%; Score 5; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AALPR 7
Db 7 AALPR 11

RESULT 24

US-08-532-818-46
Sequence 46, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
Constraining Groups Which Flank A Protein-Protein Interactio
TITLE OF INVENTION: Site
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-532-818-46

Query Match 20.0%; Score 5; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AALPR 7
Db 7 AALPR 11

RESULT 25

US-09-231-797-46
Sequence 46, Application US/09231797
Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha

US-09-207-621-46

Query Match 20.0%; Score 5; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AALPR 7
Db 7 AALPR 11

RESULT 23

US-09-207-621-46
Sequence 46, Application US/09207621
Patent No. 5952465
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
Constraining Groups Which Flank A Protein-Protein Interaction S
TITLE OF INVENTION: Site
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-933-402-46

Query Match 20.0%; Score 5; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AALPR 7
Db 7 AALPR 11

US-09-207-621-46

Query Match 20.0%; Score 5; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AALPR 7
Db 7 AALPR 11

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

TITLE OF INVENTION: Polypeptides That Include Conformation-
 Constraining Groups Which Flank A Protein-Protein Interaction
 NUMBER OF SEQUENCES: 153
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: Suite 500, 3000 K Street NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20007
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/09/231,797
 FILING DATE:
 APPLICATION NUMBER: 08/532,818
 FILING DATE: 03-MAY-1996
 APPLICATION NUMBER: PCT/US94/04294
 FILING DATE: 21-APR-1994
 PRIOR APPLICATION DATA: U.S. 08/143,364
 APPLICATION NUMBER: U.S. 08/143,364
 FILING DATE: 29-OCT-1993
 PRIOR APPLICATION DATA: U.S. 08/051,741
 APPLICATION NUMBER: U.S. 08/051,741
 FILING DATE: 23-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Isaacson, John P.
 REGISTRATION NUMBER: 33,751
 REFERENCE/DOCKET NUMBER: 040433/0148
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-231-797-46

Query Match 20.0%; Score 5; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
 DB 7 AALPR 11

RESULT 26
 US-08-934-224-46
 Sequence 46, Application US/08934224
 Patent No. 610044
 GENERAL INFORMATION:
 APPLICANT: EVANS, Herbert J.
 TITLE OF INVENTION: Polypeptides That Include Conformation-
 Constraining Groups Which Flank A Protein-Protein Interaction
 NUMBER OF SEQUENCES: 153
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: Suite 500, 3000 K Street NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20007
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,224
 FILING DATE:
 PRIOR APPLICATION DATA: 08/532,818
 APPLICATION NUMBER: PCT/US94/04294
 FILING DATE: 21-APR-1994
 PRIOR APPLICATION DATA: U.S. 08/143,364
 APPLICATION NUMBER: U.S. 08/143,364
 FILING DATE: 29-OCT-1993
 PRIOR APPLICATION DATA: U.S. 08/051,741
 APPLICATION NUMBER: U.S. 08/051,741
 FILING DATE: 23-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Isaacson, John P.
 REGISTRATION NUMBER: 33,751
 REFERENCE/DOCKET NUMBER: 040433/0148
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-934-224-46

Query Match 20.0%; Score 5; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
 DB 7 AALPR 11

RESULT 27
 US-08-933-843-46
 Sequence 46, Application US/08933843
 Patent No. 6111069
 GENERAL INFORMATION:
 APPLICANT: EVANS, Herbert J.
 TITLE OF INVENTION: Polypeptides That Include Conformation-
 Constraining Groups Which Flank A Protein-Protein Interaction
 NUMBER OF SEQUENCES: 153
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: Suite 500, 3000 K Street NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20007
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/933,843
 FILING DATE: 19-SEPT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/532,818
 FILING DATE: 03-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/143,364
 FILING DATE: 29-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/051,741
 FILING DATE: 23-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Isaacson, John P.
 REGISTRATION NUMBER: 33,751
 REFERENCE/DOCKET NUMBER: 040433/0148
 INFORMATION FOR SEQ ID NO: 46:

us-09-441-061-2.rai

Thu Dec 19 17:47:39 2002

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-843-46
Query Match 20.0%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AALPR 7
DB 7 AALPR 11

RESULT 28
US-08-934-223-46
; Sequence 46, Application US/08934223
; Patent No. 6147189
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-223-46
Query Match 20.0%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AALPR 7
DB 7 AALPR 11

RESULT 29
US-08-934-223-46
; Sequence 46, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-46
Query Match 20.0%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AALPR 7
DB 7 AALPR 11

RESULT 30
US-09-009-953-173
; Sequence 173, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; TITLE OF INVENTION: Reactive DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

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us-09-441-061-2.ra1

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REFERENCE/DOCKET NUMBER: 018623-011520US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-009-953-184

Query Match 20.0%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 6 RLIAF 10

RESULT 31
US-09-009-953-184
Sequence 184, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-09-009-953-173

Query Match 20.0%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 7 RLIAF 11

RESULT 31
US-09-009-953-184
Sequence 184, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762

Query Match

20.0%; Score 5; DB 4; Length 15;

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; TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-282-758B-2

Query Match 20.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 3 RLIAF 7

RESULT 35
US-09-143-124-22
; Sequence 22, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 22
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
; US-09-143-124-22

Query Match 20.0%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGAA 25
DB 12 KKGAA 16

RESULT 36
US-09-009-953-206
; Sequence 206, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR RESTRICTED EPITOPES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-282-758B-2

Query Match 20.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 3 RLIAF 7

RESULT 35
US-09-143-124-22
; Sequence 22, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 22
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
; US-09-143-124-22

Query Match 20.0%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGAA 25
DB 12 KKGAA 16

RESULT 36
US-09-009-953-206
; Sequence 206, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR RESTRICTED EPITOPES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-009-953-206

Query Match 20.0%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 10 RLIAF 14

RESULT 37
US-09-556-605-70
; Sequence 70, Application US/09556605
; Patent No. 6417324
; GENERAL INFORMATION:
; APPLICANT: Salberg, Matti
; APPLICANT: Lazdina, Una
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; FILE REFERENCE: TRIPEP.020A
; CURRENT APPLICATION NUMBER: US/09/556,605
; CURRENT FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-70

Query Match 20.0%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTSEH 15
DB 11 FTSEH 15

RESULT 38
US-09-556-605-73
; Sequence 73, Application US/09556605
; Patent No. 6417324
; GENERAL INFORMATION:
; APPLICANT: Salberg, Matti
; APPLICANT: Lazdina, Una
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; FILE REFERENCE: TRIPEP.020A
; CURRENT APPLICATION NUMBER: US/09/556,605
; CURRENT FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-73

Query Match 20.0%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTSEH 15
DB 11 FTSEH 15

RESULT 39
PCT-US92-07865-2
; Sequence 2, Application PC/TUS9207865
; GENERAL INFORMATION:
; APPLICANT: Dreeman, Gordon R.
; APPLICANT: Burk, Kenneth H.
; APPLICANT: Pauletti, Daniel
; TITLE OF INVENTION: Peptide-Based Hepatitis C Virus
; FILE REFERENCE: Immunoassays
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07865
; FILING DATE: 19920916
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: 16-SEP-1991
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 1600-0086.41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

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us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/723,425A
APPLICATION NUMBER: US/08/723,425A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-13
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HCV
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
NAME/KEY: Modified-site
LOCATION: 22
US-08-723-425A-58

Query Match 20.0%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
Db 11 RLIAF 15

RESULT 42
US-09-112-206-58
Sequence 58, Application US/09112206
Patent No. 6210903
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/09/112,206
APPLICATION NUMBER: US/09/112,206
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,028
FILING DATE:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids

ORIGINAL SOURCE: Hepatitis C Virus
ORGANISM: DP2, amino acids 1902 to 1922 of
INDIVIDUAL ISOLATE: HCV polyprotein
INDIVIDUAL ISOLATE: HCV polyprotein
PCT-US92-07865-2

Query Match 20.0%; Score 5; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
Db 17 RLIAF 21

RESULT 40
US-08-146-028-58
Sequence 58, Application US/08146028
Patent No. 5891640
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/08/146,028
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HCV
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
NAME/KEY: Modified-site
LOCATION: 22
US-08-146-028-58

Query Match 20.0%; Score 5; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
Db 11 RLIAF 15

RESULT 41
US-08-723-425A-58
Sequence 58, Application US/08723425A
Patent No. 6185730
GENERAL INFORMATION:
APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
NUMBER OF SEQUENCES: 453
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIE, P.C.

us-09-441-061-2.rai

Thu Dec 19 17:47:39 2002

```

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE: HCV
; INDIVIDUAL ISOLATE:
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 22
; US-09-112-206-58
;
Query Match 20.0%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
    |||||
Db 11 RLIAF 15

RESULT 43
5475086-9
; Patent No. 5475086
; APPLICANT: TOBIN, ALLAN J.; BERLANDER, MARK G.; KAUFMAN,
; DANIEL L.; CLARE-SALZLER, MICHAEL J.
; TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE
; PEPTIDES
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/135,849
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 716,909
; FILING DATE: 18-JUN-1991
; APPLICATION NUMBER: 586,536
; FILING DATE: 21-SEP-1990
; SEQ ID NO: 9:
; LENGTH: 23
5475086-9

Query Match 20.0%; Score 5; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALPRL 8
    |||||
Db 19 ALPRL 23

RESULT 44
US-08-592-500-36
; Sequence 36, Application US/08592500
; Patent No. 6005089
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,006
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
;

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; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,500
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..24
; OTHER INFORMATION: /note= "Tandem leu-rich repeated
; structure for platelet GPV."
; US-08-592-500-36
;
Query Match 20.0%; Score 5; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALPRL 8
    |||||
Db 12 ALPRL 16

RESULT 45
US-08-195-006-36
; Sequence 36, Application US/08195006
; Patent No. 6083688
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,006
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
;

```


us-09-441-061-2-rai

Thu Dec 19 17:47:39 2002

Query Match 20.0%; Score 5; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 7 RLIAF 11
DB 2 RLIAF 6

RESULT 47
PCT-US94-07644A-36
Sequence 36, Application PC/TUS9407644A
GENERAL INFORMATION:
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07644A
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 012418-003000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..24
OTHER INFORMATION: /note= "Tandem leu-rich repeated structure for platelet GPV."
FILING DATE: 19920916
PCT-US94-07644A-36

QY 4 ALPRL 8
DB 12 ALPRL 16

Query Match 20.0%; Score 5; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 4 ALPRL 8
DB 12 ALPRL 16

RESULT 48
US-08-452-242-1
Sequence 1, Application US/08452242
Patent No. 5935795
GENERAL INFORMATION:
APPLICANT: LIN LEU-PEN; COLLINS, FRANKLIN D.;
APPLICANT: DOHERTY, DANIEL H.; LILE, JACK; BEKTESH,
APPLICANT: SUSAN
TITLE OF INVENTION: Glial Derived Neurotrophic Factor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200

QY 4 ALPRL 8
DB 12 ALPRL 16

Query Match 20.0%; Score 5; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 4 ALPRL 8
DB 12 ALPRL 16

RESULT 49
US-08-452-242-1
Sequence 1, Application US/08452242
Patent No. 5935795
GENERAL INFORMATION:
APPLICANT: LIN LEU-PEN; COLLINS, FRANKLIN D.;
APPLICANT: DOHERTY, DANIEL H.; LILE, JACK; BEKTESH,
APPLICANT: SUSAN
TITLE OF INVENTION: Glial Derived Neurotrophic Factor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200

QY 4 ALPRL 8
DB 12 ALPRL 16

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..24
OTHER INFORMATION: /note= "Tandem leu-rich repeated structure for platelet GPV."
US-08-195-006-36

Query Match 20.0%; Score 5; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 4 ALPRL 8
DB 12 ALPRL 16

RESULT 46
PCT-US92-07865-3

Sequence 3, Application PC/TUS9207865
GENERAL INFORMATION:
APPLICANT: Dreesman, Gordon R.
APPLICANT: Burk, Kenneth H.
APPLICANT: Pauletti, Daniel
TITLE OF INVENTION: Peptide-Based Hepatitis C Virus
TITLE OF INVENTION: Immunoassays
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07865
FILING DATE: 19920916
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 16-SEP-1991
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 1600-0086.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Hepatitis C Virus
INDIVIDUAL ISOLATE: DP3, amino acids 1917 to 1940 of the
INDIVIDUAL ISOLATE: HCV polyprotein

QY 4 ALPRL 8
DB 12 ALPRL 16

Query Match 20.0%; Score 5; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 4 ALPRL 8
DB 12 ALPRL 16

RESULT 47
PCT-US92-07865-3
Sequence 3, Application PC/TUS9207865
GENERAL INFORMATION:
APPLICANT: Dreesman, Gordon R.
APPLICANT: Burk, Kenneth H.
APPLICANT: Pauletti, Daniel
TITLE OF INVENTION: Peptide-Based Hepatitis C Virus
TITLE OF INVENTION: Immunoassays
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07865
FILING DATE: 19920916
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 16-SEP-1991
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 1600-0086.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Hepatitis C Virus
INDIVIDUAL ISOLATE: DP3, amino acids 1917 to 1940 of the
INDIVIDUAL ISOLATE: HCV polyprotein

QY 4 ALPRL 8
DB 12 ALPRL 16

Query Match 20.0%; Score 5; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 4 ALPRL 8
DB 12 ALPRL 16

RESULT 48
PCT-US92-07865-3
Sequence 3, Application PC/TUS9207865
GENERAL INFORMATION:
APPLICANT: Dreesman, Gordon R.
APPLICANT: Burk, Kenneth H.
APPLICANT: Pauletti, Daniel
TITLE OF INVENTION: Peptide-Based Hepatitis C Virus
TITLE OF INVENTION: Immunoassays
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07865
FILING DATE: 19920916
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 16-SEP-1991
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 1600-0086.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Hepatitis C Virus
INDIVIDUAL ISOLATE: DP3, amino acids 1917 to 1940 of the
INDIVIDUAL ISOLATE: HCV polyprotein

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

CITY: Englewood
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/452,242
 FILING DATE: 26-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/182,183
 FILING DATE: 23-MAY-1994
 APPLICATION NUMBER: 07/788,423
 FILING DATE: 06-NOV-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/774,109
 FILING DATE: 08-OCT-1991
 APPLICATION NUMBER: 07/764,685
 FILING DATE: 20-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/855,413
 FILING DATE: 19-MARCH-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: SYNE-225C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 FRAGMENT TYPE: N-terminal fragment
 US-08-452-242-1

Query Match 20.0%; Score 5; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
 DB 7 AALPR 11

RESULT 49
 US-08-934-741A-23
 Sequence 23, Application US/08934741A
 Patent No. 5977298
 GENERAL INFORMATION:
 APPLICANT: Shibata, Kenji
 APPLICANT: Yamasaki, Motoo
 APPLICANT: Yamada, Masako
 APPLICANT: Tamaoki, Tatsuya
 APPLICANT: Kosaka, No. 5977298uo
 APPLICANT: Sato, Soichiro
 TITLE OF INVENTION: NOVEL CALCITONIN DERIVATIVES
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Antonelli, Terry, Stout, & Kraus, LLP
 STREET: Suite 1800, 1300 No. 5977298th Seventeenth Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22209
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM-PC
 OPERATING SYSTEM: DOS
 SOFTWARE: Word Perfect; Version #5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,741A
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 061026/95
 FILING DATE: 20-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Solomon, William I.
 REGISTRATION NUMBER: 28,565
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-312-6600
 TELEFAX: 703-312-6666
 TELEX:
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 25
 IDENTIFICATION METHOD: by experiment
 OTHER INFORMATION: /label=Xaa at location 25
 OTHER INFORMATION: /note= L-prolinamide
 US-08-934-741A-23

Query Match 20.0%; Score 5; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
 DB 13 AALPR 17

RESULT 50
 US-08-453-176A-1
 Sequence 1, Application US/08453176A
 Patent No. 6015572
 GENERAL INFORMATION:
 APPLICANT: LIN, LEU-PEN
 APPLICANT: COLLINS, FRANKLIN D.
 APPLICANT: DOHERTY, DANIEL H.
 APPLICANT: LILE, JACK
 APPLICANT: BEKTESH, SUSAN
 TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AMGEN INC.
 STREET: One Amgen Center Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: 7.1
 SOFTWARE: Microsoft Word for WIN 7.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/453,176A
 FILING DATE:
 INFORMATION FOR SEQ ID NO: 1:
 INFORMATION FOR SEQ ID NO: 1:

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic

TITLE OF INVENTION: Factor

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word for WIN 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,268A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/453,176

FILING DATE:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

FRAGMENT TYPE: N-terminal fragment

US-08-935-268A-1

Query Match 20.0%; Score 5; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7

DB 7 AALPR 11

RESULT 53

US-08-452-229-1

Sequence 1, Application US/08452229

Patent No. 6362319

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: 1840 DeHavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: Macintosh

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/452,229

FILING DATE: 26-MAY-1995

PRIOR APPLICATION DATA: 530

APPLICATION NUMBER: 08/182,183

FILING DATE: 23-MAY-1994

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

QY 3 AALPR 7

DB 7 AALPR 11

RESULT 52

US-08-935-268A-1

Sequence 1, Application US/08935268A

Patent No. 6221376

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word for WIN 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,374

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/182,183

FILING DATE: 23-MAY-1994

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

QY 3 AALPR 7

DB 7 AALPR 11

RESULT 51

US-08-451-374-1

Sequence 1, Application US/08451374

Patent No. 6093802

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic

Factor

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word for WIN 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,374

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/182,183

FILING DATE: 23-MAY-1994

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

FRAGMENT TYPE: N-terminal fragment

US-08-451-374-1

Query Match 20.0%; Score 5; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7

DB 7 AALPR 11

RESULT 50

US-08-451-374-1

Sequence 1, Application US/08451374

Patent No. 6093802

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic

Factor

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word for WIN 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,374

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/182,183

FILING DATE: 23-MAY-1994

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

FRAGMENT TYPE: N-terminal fragment

US-08-451-374-1

Query Match 20.0%; Score 5; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7

DB 7 AALPR 11

RESULT 49

US-08-451-374-1

Sequence 1, Application US/08451374

Patent No. 6093802

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic

Factor

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word for WIN 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,374

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/182,183

FILING DATE: 23-MAY-1994

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

FRAGMENT TYPE: N-terminal fragment

US-08-451-374-1

Query Match 20.0%; Score 5; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7

DB 7 AALPR 11

RESULT 48

US-08-451-374-1

Sequence 1, Application US/08451374

Patent No. 6093802

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic

Factor

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word for WIN 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,374

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/182,183

FILING DATE: 23-MAY-1994

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

FRAGMENT TYPE: N-terminal fragment

US-08-451-374-1

Query Match 20.0%; Score 5; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7

DB 7 AALPR 11

RESULT 47

US-08-451-374-1

Sequence 1, Application US/08451374

Patent No. 6093802

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

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; TOPOLOGY: linear
; FRAGMENT TYPE: N-terminal fragment
US-08-452-229-1
    Query Match      20.0%; Score 5; DB 4; Length 25;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0;
    Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 3 AALPR 7
    |||||
DB 7 AALPR 11

RESULT 54
US-08-785-247-6
; Sequence 6, Application US/08785247
; Patent No. 6040149
; GENERAL INFORMATION:
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Liu, Jun
; APPLICANT: Zhang, Yuhua
; TITLE OF INVENTION: ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
; TITLE OF INVENTION: CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
; TITLE OF INVENTION: SUPPRESSOR OF RAS, AND METHODS OF USING SAID AGENTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,247
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 28,678
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 48582-A/JPW/CCA
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-381-0526
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-785-247-6
    Query Match      16.0%; Score 4; DB 3; Length 4;
    Best Local Similarity 100.0%; Pred. No. 1.9e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
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DB 1 AALP 4

RESULT 55
US-08-484-192-2
; Sequence 2, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APATERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-484-192-2
    Query Match      16.0%; Score 4; DB 1; Length 6;
    Best Local Similarity 100.0%; Pred. No. 1.9e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRLI 9
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DB 2 PRLI 5

Search completed: December 19, 2002, 17:44:23
Job time : 15 secs

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us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

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QM protein - protein search, using sw model

Run on: December 19, 2002, 17:43:10 ; Search time 11 seconds
(without alignments)
38.039 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25
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Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 106657 seqs, 16763532 residues

Word size : 0
Total number of hits satisfying chosen parameters: 36679

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

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14: /cgn2_6/ptodata/2/pubaa/US60 PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 25 | 20.0 | 9 | 10 | US-09-894-018-213 |
| 3 | 5 | 20.0 | 15 | 9 | US-10-074-257-6 |
| 4 | 5 | 20.0 | 21 | 10 | US-09-839-447A-70 |
| 5 | 5 | 20.0 | 21 | 10 | US-09-839-447A-73 |
| 6 | 5 | 20.0 | 21 | 10 | US-09-917-340-24 |
| 7 | 5 | 20.0 | 25 | 10 | US-09-864-761-34001 |
| 8 | 4 | 16.0 | 8 | 9 | US-09-826-230-363 |
| 9 | 4 | 16.0 | 8 | 10 | US-09-244-694-186 |
| 10 | 4 | 16.0 | 9 | 10 | US-09-739-307-101 |
| 11 | 4 | 16.0 | 9 | 10 | US-09-760-599-7 |
| 12 | 4 | 16.0 | 9 | 10 | US-09-760-599-23 |
| 13 | 4 | 16.0 | 9 | 10 | US-09-005-243-69 |
| 14 | 4 | 16.0 | 9 | 10 | US-09-224-683-69 |
| 15 | 4 | 16.0 | 9 | 10 | US-09-834-765-30 |
| 16 | 4 | 16.0 | 4 | 16.0 | US-08-424-550B-278 |
| 17 | 4 | 16.0 | 10 | 10 | US-09-834-765-65 |
| 18 | 4 | 16.0 | 10 | 10 | US-09-834-765-305 |
| 19 | 4 | 16.0 | 10 | 10 | US-09-922-261-9 |

ALIGNMENTS

RESULT 1
US-08-981-824-29
; Sequence 29, Application US/08981824
; Patent No. US20020114816A1
; GENERAL INFORMATION:
; APPLICANT: ENDL, Josef
; APPLICANT: STAHL, Peter
; APPLICANT: ALBERT, Winfried
; APPLICANT: SCHENDEL, Dolores
; APPLICANT: BOITARD, Christian
; APPLICANT: VAN ENDERT, Peter
; APPLICANT: JUNG, Gunther-Gerhard

| | | | | | | |
|----|---|------|----|----|---------------------|--------------------|
| 20 | 4 | 16.0 | 11 | 10 | US-09-984-056-86 | Sequence 86, Appl |
| 21 | 4 | 16.0 | 11 | 10 | US-09-984-057-86 | Sequence 86, Appl |
| 22 | 4 | 16.0 | 11 | 10 | US-09-873-459A-37 | Sequence 37, Appl |
| 23 | 4 | 16.0 | 12 | 10 | US-09-879-257A-4 | Sequence 4, Appl |
| 24 | 4 | 16.0 | 12 | 10 | US-09-765-614B-16 | Sequence 16, Appl |
| 25 | 4 | 16.0 | 12 | 10 | US-09-925-715-17 | Sequence 17, Appl |
| 26 | 4 | 16.0 | 12 | 10 | US-09-909-950-10 | Sequence 10, Appl |
| 27 | 4 | 16.0 | 12 | 10 | US-09-871-838-191 | Sequence 191, Appl |
| 28 | 4 | 16.0 | 13 | 10 | US-09-895-072-52 | Sequence 52, Appl |
| 29 | 4 | 16.0 | 13 | 10 | US-09-986-352-52 | Sequence 11, Appl |
| 30 | 4 | 16.0 | 13 | 12 | US-10-156-820-11 | Sequence 11, Appl |
| 31 | 4 | 16.0 | 14 | 10 | US-09-873-459A-38 | Sequence 38, Appl |
| 32 | 4 | 16.0 | 14 | 10 | US-09-883-825-29 | Sequence 29, Appl |
| 33 | 4 | 16.0 | 15 | 10 | US-09-731-171-82 | Sequence 82, Appl |
| 34 | 4 | 16.0 | 15 | 10 | US-09-894-018-272 | Sequence 272, Appl |
| 35 | 4 | 16.0 | 15 | 10 | US-09-972-105-1 | Sequence 82, Appl |
| 36 | 4 | 16.0 | 16 | 9 | US-09-805-301-82 | Sequence 15, Appl |
| 37 | 4 | 16.0 | 16 | 10 | US-09-746-742-15 | Sequence 15, Appl |
| 38 | 4 | 16.0 | 16 | 10 | US-09-746-742-16 | Sequence 16, Appl |
| 39 | 4 | 16.0 | 16 | 10 | US-09-746-742-18 | Sequence 18, Appl |
| 40 | 4 | 16.0 | 17 | 9 | US-09-984-245-297 | Sequence 297, Appl |
| 41 | 4 | 16.0 | 17 | 9 | US-09-996-634-95 | Sequence 95, Appl |
| 42 | 4 | 16.0 | 17 | 9 | US-09-996-634-95 | Sequence 95, Appl |
| 43 | 4 | 16.0 | 17 | 10 | US-09-729-402-1 | Sequence 1, Appl |
| 44 | 4 | 16.0 | 18 | 9 | US-09-117-846-46 | Sequence 46, Appl |
| 45 | 4 | 16.0 | 18 | 10 | US-09-864-761-3272 | Sequence 3272, A |
| 46 | 4 | 16.0 | 18 | 10 | US-09-746-742-17 | Sequence 17, Appl |
| 47 | 4 | 16.0 | 18 | 10 | US-09-746-742-19 | Sequence 19, Appl |
| 48 | 4 | 16.0 | 18 | 10 | US-09-746-742-38 | Sequence 38, Appl |
| 49 | 4 | 16.0 | 18 | 10 | US-09-746-742-39 | Sequence 39, Appl |
| 50 | 4 | 16.0 | 18 | 10 | US-09-746-742-40 | Sequence 40, Appl |
| 51 | 4 | 16.0 | 18 | 10 | US-09-746-742-41 | Sequence 41, Appl |
| 52 | 4 | 16.0 | 18 | 10 | US-09-746-742-55 | Sequence 55, Appl |
| 53 | 4 | 16.0 | 18 | 10 | US-09-746-742-64 | Sequence 64, Appl |
| 54 | 4 | 16.0 | 18 | 10 | US-09-746-742-65 | Sequence 65, Appl |
| 55 | 4 | 16.0 | 18 | 10 | US-09-746-742-67 | Sequence 67, Appl |
| 56 | 4 | 16.0 | 18 | 10 | US-09-746-742-68 | Sequence 68, Appl |
| 57 | 4 | 16.0 | 19 | 10 | US-09-864-761-35260 | Sequence 35260, A |
| 58 | 4 | 16.0 | 19 | 10 | US-09-864-761-36761 | Sequence 36761, A |
| 59 | 4 | 16.0 | 19 | 10 | US-09-864-761-39096 | Sequence 39096, A |
| 60 | 4 | 16.0 | 20 | 9 | US-09-938-437-2 | Sequence 2, Appl |
| 61 | 4 | 16.0 | 20 | 10 | US-09-746-742-43 | Sequence 43, Appl |
| 62 | 4 | 16.0 | 20 | 10 | US-09-746-742-45 | Sequence 45, Appl |
| 63 | 4 | 16.0 | 20 | 10 | US-09-746-742-46 | Sequence 46, Appl |
| 64 | 4 | 16.0 | 20 | 10 | US-09-746-742-48 | Sequence 48, Appl |
| 65 | 4 | 16.0 | 20 | 10 | US-09-746-742-49 | Sequence 49, Appl |
| 66 | 4 | 16.0 | 20 | 10 | US-09-746-742-51 | Sequence 51, Appl |
| 67 | 4 | 16.0 | 20 | 10 | US-09-746-742-53 | Sequence 53, Appl |
| 68 | 4 | 16.0 | 20 | 10 | US-09-746-742-56 | Sequence 56, Appl |
| 69 | 4 | 16.0 | 20 | 10 | US-09-746-742-66 | Sequence 66, Appl |
| 70 | 4 | 16.0 | 21 | 9 | US-10-012-896-986 | Sequence 986, Appl |
| 71 | 4 | 16.0 | 21 | 10 | US-09-864-761-33410 | Sequence 33410, A |
| 72 | 4 | 16.0 | 22 | 9 | US-10-117-057-10 | Sequence 10, Appl |
| 73 | 4 | 16.0 | 22 | 10 | US-09-005-243-75 | Sequence 75, Appl |
| 74 | 4 | 16.0 | 22 | 10 | US-09-005-243-75 | Sequence 75, Appl |
| 75 | 4 | 16.0 | 22 | 10 | US-09-224-683-75 | Sequence 75, Appl |

us-09-441-061-2.rapb

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TITLE OF INVENTION: AUTOREACTIVE PEPTIDES FROM HUMAN GLUTAMIC ACID

TITLE OF INVENTION: DECARBOXYLASE (GAD)
 FILE REFERENCE: 564-7029
 CURRENT APPLICATION NUMBER: US/08/981,824
 CURRENT FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: PCT/EP96/03093
 EARLIER FILING DATE: 1996-07-15
 EARLIER APPLICATION NUMBER: DE/195 25 784.7
 EARLIER FILING DATE: 1995-07-14
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 29
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-981-824-29

Query Match 100.0%; Score 25; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7e-20;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSEHSHFSLKKGAA 25
 DB 1 GMAALPRLIAFTSEHSHFSLKKGAA 25

RESULT 2
 US-09-894-018-213
 Sequence 213, Application US/09894018
 Patent No. US20020119127A1
 GENERAL INFORMATION:
 APPLICANT: EPIMUNE, Inc.
 APPLICANT: Sette, Alessandro
 APPLICANT: Chestnut, Robert
 APPLICANT: Livingston, Brian
 APPLICANT: Baker, Deniaw
 APPLICANT: Newman, Mark
 APPLICANT: Brown, David
 TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
 TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
 FILE REFERENCE: 39963-20033.00
 CURRENT APPLICATION NUMBER: US/09/894,018
 CURRENT FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: PCT/US00/35568
 PRIOR FILING DATE: 2000-12-28
 PRIOR APPLICATION NUMBER: US 60/173,390
 PRIOR FILING DATE: 1999-12-28
 OR APPLICATION NUMBER: US 60/284,221
 OR FILING DATE: 2001-04-15
 NUMBER OF SEQ ID NOS: 368
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 213
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Transgenic mouse
 US-09-894-018-213

Query Match 20.0%; Score 5; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
 DB 4 RLIAF 8

RESULT 3
 US-10-074-257-6
 Sequence 6, Application US/10074257
 Publication No. US20020187147A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Chih-Pin
 APPLICANT: Lin, Wei-Jen

TITLE OF INVENTION: Antigen Specific Recombinant MHC Class II Molecules and Methods
 FILE REFERENCE: 1954-313
 CURRENT APPLICATION NUMBER: US/10/074,257
 CURRENT FILING DATE: 2002-06-18
 PRIOR APPLICATION NUMBER: US 60/268,714
 PRIOR FILING DATE: 2001-02-15
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patent in version 3.0
 SEQ ID NO 6
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo Sapiens and Mus musculus
 US-10-074-257-6

Query Match 20.0%; Score 5; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGAA 25
 DB 1 KKGAA 5

RESULT 4
 US-09-839-447A-70
 Sequence 70, Application US/09839447A
 Patent No. US20020058247A1
 GENERAL INFORMATION:
 APPLICANT: Salberg, Matti
 TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
 TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
 FILE REFERENCE: TRIPEP.020CP1
 CURRENT APPLICATION NUMBER: US/09/839,447A
 CURRENT FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/556605
 PRIOR FILING DATE: 2000-04-21
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 70
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Artificial Peptide
 US-09-839-447A-70

Query Match 20.0%; Score 5; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTSEH 15
 DB 11 FTSEH 15

RESULT 5
 US-09-839-447A-73
 Sequence 73, Application US/09839447A
 Patent No. US20020058247A1
 GENERAL INFORMATION:
 APPLICANT: Salberg, Matti
 TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
 TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
 FILE REFERENCE: TRIPEP.020CP1
 CURRENT APPLICATION NUMBER: US/09/839,447A
 CURRENT FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/556605
 PRIOR FILING DATE: 2000-04-21
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 73
 LENGTH: 21
 TYPE: PRT

us-09-441-061-2.rapb

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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-09-839-447A-73

Query Match 20.0%; Score 5; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FTSEH 15
Db 12 FTSEH 16

RESULT 6
US-09-917-340-24
Sequence 24, Application US/09917340
Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TELANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 24
LENGTH: 21
TYPE: PRT
ORGANISM: Misgurnus Anguillicaudatus
US-09-917-340-24

Query Match 20.0%; Score 5; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 KGA 25
Db 12 KGA 16

RESULT 7
US-09-864-761-34001
Sequence 34001, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34001
LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006017.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HEL1, SIGNAL = 18
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 13
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 18
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 13
OTHER INFORMATION: EST_HUMAN HIT: AA332025.1, EVALUATE 4.00e-08
OTHER INFORMATION: EST_HUMAN HIT: AW965281.1, EVALUATE 3.00e-08
US-09-864-761-34001

Query Match 20.0%; Score 5; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 SEHSH 17
Db 14 SEHSH 18

RESULT 8
US-09-826-290-363
Sequence 363, Application US/09826290
Patent No. US20020164668A1
GENERAL INFORMATION:
APPLICANT: Durham, L. Kathryn
APPLICANT: Friedman, David L.
APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
APPLICANT: Kimmel, Lida H.
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Potter, David M.
APPLICANT: Rohlf, Christian
APPLICANT: Silber, B. Michael
APPLICANT: Stiger, Thomas R.
APPLICANT: Sunderland, P. Trey
APPLICANT: Townsend, Robert Reid

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

```

; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 363
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-363

; Query Match
; Best Local Similarity 16.0%; Score 4; DB 9; Length 8;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAAL 5
Db 4 MAAL 7

RESULT 9
US-09-244-694-186
; Sequence 186, Application US/09244694
; Patent No. US2002026037A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; APPLICANT: Olsen, Henrik S.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 3
; FILE REFERENCE: 1488.1040003
; CURRENT APPLICATION NUMBER: US/09/244,694
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 09/132,088
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: US 09/033,662
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: US 08/469,641
; EARLIER FILING DATE: 1995-06-06
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 186
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-244-694-186

; Query Match
; Best Local Similarity 16.0%; Score 4; DB 10; Length 8;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAAL 5
Db 1 MAAL 4

RESULT 10
US-09-739-907-101
; Sequence 101, Application US/09739907
; Patent No. US2001001288A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2022P1
; CURRENT APPLICATION NUMBER: US/09/739,907

```

```

; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/348,457
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; PRIOR FILING DATE: 1998-01-07
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-739-907-101

; Query Match
; Best Local Similarity 16.0%; Score 4; DB 10; Length 9;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 11
US-09-760-599-7
; Sequence 7, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1C1P
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-760-599-7

; Query Match
; Best Local Similarity 16.0%; Score 4; DB 10; Length 9;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRLI 9
Db 5 PRLI 8

RESULT 12
US-09-760-599-23
; Sequence 23, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1C1P
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

```


us-09-441-061-2.rapb

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-760-599-23

Query Match 16.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRLI 9
DB 5 PRLI 8

RESULT 13
US-09-005-243-69
Sequence 69, Application US/09005243
Patent No. US2002018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0448
TELEFAX: 312/474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-005-243-69

Query Match 16.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 2 SLKK 5

RESULT 14
US-09-224-683-69
Sequence 69, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids

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;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-224-683-69
;
; Query Match
; Best Local Similarity 16.0%; Score 4; DB 10; Length 9;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 19 SLKK 22
Db 2 SLKK 5
;
; RESULT 15
; US-09-834-765-30
; Sequence 30, Application US/09834765
; Patent No. US20020055478A1
; TRAL INFORMATION:
; ELICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovics
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-834-765-30

```

```

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 LPLR 8
Db 3 LPLR 6
;
; RESULT 17
; US-09-834-765-65
; Sequence 65, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovics
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-834-765-65

```

```

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 PRLI 9
Db 4 PRLI 7
;
; RESULT 16
; US-08-424-550B-278
; Sequence 278, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL

```

```

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 PRLI 9
Db 4 PRLI 7
;
; RESULT 18
; US-09-834-765-305
; Sequence 305, Application US/09834765

```

```

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 PRLI 9
Db 4 PRLI 7
;
; RESULT 18
; US-09-834-765-305
; Sequence 305, Application US/09834765

```

```

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 PRLI 9
Db 4 PRLI 7
;
; RESULT 18
; US-09-834-765-305
; Sequence 305, Application US/09834765

```

```

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 PRLI 9
Db 4 PRLI 7
;
; RESULT 18
; US-09-834-765-305
; Sequence 305, Application US/09834765

```

```

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

```

; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Paris
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USUL
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-834-765-305

```

```

Query Match 16.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 6 PRLI 9
    ||||
Db 4 PRLI 7

```

```

RESULT 19
US-09-922-261-9
; Sequence 9, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo. Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kaeturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-922-261-9

```

```

Query Match 16.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 AALP 6
    ||||
Db 3 AALP 6

```

```

RESULT 20
US-09-984-056-86
; Sequence 86, Application US/09984056
; Patent No. US20020120106A1

```

```

; GENERAL INFORMATION:
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: ANTHRAZ AND SMALL POX REPLICINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 86
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-984-056-86

```

```

Query Match 16.0%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 ALPR 7
    ||||
Db 7 ALPR 10

```

```

RESULT 21
US-09-984-057-86
; Sequence 86, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
; TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 86
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-984-057-86

```

```

Query Match 16.0%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 ALPR 7
    ||||
Db 7 ALPR 10

```

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```

; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Dabsyl-Tyr
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: RGDS chain linked via NH2 group
; OTHER INFORMATION: of lysine
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Branched core
; OTHER INFORMATION: peptide comprising a dabsylated
; OTHER INFORMATION: atherosclerotic
; OTHER INFORMATION: plaque-binding sequence and
; OTHER INFORMATION: RGDS
; US-09-765-614B-16

```

```

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 20 LKKG 23
Db 8 LKKG 11

```

```

RESULT 25
US-09-925-715-17
; Sequence 17, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Core peptide
; OTHER INFORMATION: comprising dabsylated-atherosclerotic plaque
; OTHER INFORMATION: binding sequence and RGDS
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Dabsylated-tyrosine
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Arg-Gly-Asp-Ser chain linked via NH2 group of
; OTHER INFORMATION: lysine
; US-09-925-715-17

```

```

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 20 LKKG 23
Db 8 LKKG 11

```

```

; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HBV
; OTHER INFORMATION: capsid-binding peptide
; US-09-873-459A-37

```

```

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 22 KGAA 25
Db 9 KGAA 12

```

```

RESULT 23
US-09-879-257A-4
; Sequence 4, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-879-257A-4

```

```

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 20 LKKG 23
Db 1 LKKG 4

```

```

RESULT 24
US-09-765-614B-16
; Sequence 16, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic

```

RESULT 26

US-09-909-950-10
; Sequence 10, Application US/09909950
; Patent No. US20020111299A1
; GENERAL INFORMATION:
; APPLICANT: KOLBER, Hanno V.J.
; RASMUSSEN, Ulla B.
; KREIL, Gunther
; ACHETTER, Tilman
; TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/909,950
; FILING DATE: 23-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/909,950
; FILING DATE: 2001-01-23
; APPLICATION NUMBER: FR 90 07901
; FILING DATE: 29-JUN-1993
; APPLICATION NUMBER: FR 94 00202
; FILING DATE: 11-JAN-1994
; APPLICATION NUMBER: FR 9400062.9
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 017753-071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6520
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..12
; OTHER INFORMATION: /note= "xenoxin-1, alkylated,
; fragment C1(2)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-909-950-10

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 1 SLKK 4

RESULT 27

US-09-071-838-191
; Sequence 191, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:

APPLICANT: Fischer, Robert L.
APPLICANT: Chad, Nir, Tomohiro
APPLICANT: Kiyosue, Ramin
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/071,838
FILING DATE: 01-May-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-071-838-191

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 4 SLKK 7

RESULT 28

US-09-895-072-52
; Sequence 52, Application US/09895072
; Patent No. US200202550A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM M
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 210119US0CONT
; CURRENT APPLICATION NUMBER: US/09/895,072
; PRIOR FILING DATE: 2001-07-02
; PRIOR FILING DATE: 1999-09-14
; PRIOR FILING DATE: 1999-09-14
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-072-52

Query Match 16.0%; Score 4; DB 10; Length 13;

us-09-441-061-2.rapb

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Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRLI 9
|
|
|
|
Db 6 PRLI 9

RESULT 29
US-09-986-552-52
; Sequence 52, Application US/09986552
; Patent No. US20020150981A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 215098US77DIV
; CURRENT APPLICATION NUMBER: US/09/986,552
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/635,872
; FOR FILING DATE: 2000-08-10
; FOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-552-52

Query Match 16.0%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRLI 9
|
|
|
|
Db 6 PRLI 9

RESULT 30
US-10-156-820-11
; Sequence 11, Application US/10156820
; Patent No. US20020150558A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mastadenovirus, serotype 2
US-10-156-820-11

Query Match 16.0%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
|
|
|
|
Db 3 SLKK 6

RESULT 31
US-09-873-459A-38
; Sequence 38, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Muiray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-38

Query Match 16.0%; Score 4; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGAA 25
|
|
|
|
Db 10 KGAA 13

RESULT 32
US-09-883-825-29
; Sequence 29, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991

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Patent No. US20020119127A1
 GENERAL INFORMATION:
 APPLICANT: EPIMUNE, Inc.
 APPLICANT: Sette, Alessandro
 APPLICANT: Chestnut, Robert
 APPLICANT: Livingston, Brian
 APPLICANT: Baker, Denis
 APPLICANT: Newman, Mark
 APPLICANT: Brown, David
 TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
 FILE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
 FILE REFERENCE: 39963-20033.00
 CURRENT APPLICATION NUMBER: US/09/894,018
 CURRENT FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: PCT/US00/35568
 PRIOR FILING DATE: 2000-12-28
 PRIOR APPLICATION NUMBER: US 60/173,390
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: US 60/284,221
 PRIOR FILING DATE: 2001-04-16
 NUMBER OF SEQ ID NOS: 368
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 272
 LENGTH: 15
 TYPE: PRT
 ORGANISM: P. falciparum
 US-09-894-018-272

Query Match 16.0%; Score 4; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 19 SLKK 22
 DB 12 SLKK 15

RESULT 35
 US-09-972-105-1
 Sequence 1, Application US/09972105
 Patent No. US20020127616A1
 GENERAL INFORMATION:
 APPLICANT: Burchell, Ann
 APPLICANT: Hume, Robert
 TITLE OF INVENTION: Prenatal Diagnostic Methods
 FILE OF INVENTION: Cross-References
 FILE REFERENCE: 350013-76
 CURRENT APPLICATION NUMBER: US/09/972,105
 CURRENT FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: US 09/392,055
 PRIOR FILING DATE: 1999-09-09
 PRIOR APPLICATION NUMBER: PCT/GB98/00656
 PRIOR FILING DATE: 1998-03-03
 PRIOR APPLICATION NUMBER: US 60/067,520
 PRIOR FILING DATE: 1997-12-04
 PRIOR APPLICATION NUMBER: GB 9704876.3
 PRIOR FILING DATE: 1997-03-08
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Human
 US-09-972-105-1

Query Match 16.0%; Score 4; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 19 SLKK 22
 DB 11 SLKK 14

ATTORNEY/AGENT INFORMATION:
 NAME: NO. US20020151024Aland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/30822
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 US-09-883-825-29

Query Match 16.0%; Score 4; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 19 SLKK 22
 DB 11 SLKK 14

RESULT 33
 US-09-791-171-82
 Sequence 82, Application US/09791171
 Patent No. US20020094336A1
 GENERAL INFORMATION:
 APPLICANT: ANDERSEN, Peter
 APPLICANT: NIELSEN, Rikke
 APPLICANT: OETTINGER, Thomas
 APPLICANT: RASMUSSEN, Peter Birk
 APPLICANT: ROSENKRANDS, Ida
 APPLICANT: WELDLING, Karin
 APPLICANT: FLORIO, Walter
 TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
 FILE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
 FILE REFERENCE: 670001-2002.1
 CURRENT APPLICATION NUMBER: US/09/791,171
 CURRENT FILING DATE: 2001-02-20
 PRIOR APPLICATION NUMBER: 09/050,739
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 0376/97
 PRIOR FILING DATE: 1997-04-02
 PRIOR APPLICATION NUMBER: 1277/97
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/044,624
 PRIOR FILING DATE: 1997-04-18
 PRIOR APPLICATION NUMBER: 60/070,488
 PRIOR FILING DATE: 1998-01-05
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 82
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Mycobacterium tuberculosis
 US-09-791-171-82

Query Match 16.0%; Score 4; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 AALP 6
 DB 8 AALP 11

RESULT 34
 US-09-894-018-272
 Sequence 272, Application US/09894018

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

/ CURRENT APPLICATION NUMBER: US/09/746,742
 / CURRENT FILING DATE: 2000-12-21
 / PRIOR APPLICATION NUMBER: PCT/US99/17351
 / PRIOR FILING DATE: 1999-07-30
 / PRIOR APPLICATION NUMBER: US 60/043,280
 / PRIOR FILING DATE: 1997-04-17
 / PRIOR APPLICATION NUMBER: US 09/062,241
 / PRIOR FILING DATE: 1998-04-17
 / PRIOR APPLICATION NUMBER: US 60/094,676
 / PRIOR FILING DATE: 1998-07-30
 / PRIOR APPLICATION NUMBER: US 60/100,265
 / PRIOR FILING DATE: 1998-09-14
 / PRIOR APPLICATION NUMBER: US 60/101,058
 / PRIOR FILING DATE: 1998-09-18
 / PRIOR APPLICATION NUMBER: US 60/132,295
 / PRIOR FILING DATE: 1999-05-03
 / NUMBER OF SEQ ID NOS: 68
 / SOFTWARE: Fast-SEQ for Windows Version 4.0
 / SEQ ID NO 15
 / LENGTH: 16
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: D-peptide
 / US-09-746-742-15

Query Match 16.0%; Score 4; DB 10; Length 16;
 Best Local Similarity 100.0%; Pred. No. 28+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 21 KKGK 24
 DB 1 KKGK 4

RESULT 38
 US-09-746-742-16
 / Sequence 16, Application US/09746742
 / Patent No. US20020077284A1
 / GENERAL INFORMATION:
 / APPLICANT: Eckert, Deborah M.
 / APPLICANT: Chan, David C.
 / APPLICANT: Malashkevich, Vladimir
 / APPLICANT: Carr, Peter A.
 / APPLICANT: Kim, Peter S.
 / TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
 / FILE REFERENCE: 0399.1192-008
 / CURRENT APPLICATION NUMBER: US/09/746,742
 / CURRENT FILING DATE: 2000-12-21
 / PRIOR APPLICATION NUMBER: PCT/US99/17351
 / PRIOR FILING DATE: 1999-07-30
 / PRIOR APPLICATION NUMBER: US 60/043,280
 / PRIOR FILING DATE: 1997-04-17
 / PRIOR APPLICATION NUMBER: US 09/062,241
 / PRIOR FILING DATE: 1998-04-17
 / PRIOR APPLICATION NUMBER: US 60/094,676
 / PRIOR FILING DATE: 1998-07-30
 / PRIOR APPLICATION NUMBER: US 60/100,265
 / PRIOR FILING DATE: 1998-09-14
 / PRIOR APPLICATION NUMBER: US 60/101,058
 / PRIOR FILING DATE: 1998-09-18
 / PRIOR APPLICATION NUMBER: US 60/132,295
 / PRIOR FILING DATE: 1999-05-03
 / NUMBER OF SEQ ID NOS: 68
 / SOFTWARE: Fast-SEQ for Windows Version 4.0
 / SEQ ID NO 16
 / LENGTH: 16
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: D-peptide
 / US-09-746-742-16

RESULT 36
 US-09-805-301-82
 / Sequence 82, Application US/09805301
 / Patent No. US20020173456A1
 / GENERAL INFORMATION:
 / APPLICANT: Smith, Louis C.
 / APPLICANT: Sparrow, James T.
 / APPLICANT: Hauer, Jochen
 / APPLICANT: Mims, Martha P.
 / TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 / MACROMOLECULE DELIVERY
 / NUMBER OF SEQUENCES: 139
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Lyon & Lyon
 / STREET: 633 West Fifth Street
 / SUITE: Suite 4700
 / CITY: Los Angeles
 / STATE: California
 / COUNTRY: U.S.A.
 / ZIP: 90071-2066
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: IBM P.C. DOS 6.0
 / SOFTWARE: Word Perfect 6.1
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/805,301
 / FILING DATE: 12-Mar-2001
 / CLASSIFICATION: <Unknown>
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/584,043
 / FILING DATE: <Unknown>
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Warburg, Richard J.
 / REGISTRATION NUMBER: 32,327
 / REFERENCE/DOCKET NUMBER: 217/189
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (213) 499-1600
 / TELEFAX: (213) 955-0440
 / TELEX: 67-3510
 / INFORMATION FOR SEQ ID NO: 82:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 16 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 / SEQUENCE DESCRIPTION: SEQ ID NO: 82:
 / US-09-805-301-82

Query Match 16.0%; Score 4; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 28+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
 DB 2 SLKK 5

RESULT 37
 US-09-746-742-15
 / Sequence 15, Application US/09746742
 / Patent No. US20020077284A1
 / GENERAL INFORMATION:
 / APPLICANT: Eckert, Deborah M.
 / APPLICANT: Chan, David C.
 / APPLICANT: Malashkevich, Vladimir
 / APPLICANT: Carr, Peter A.
 / APPLICANT: Kim, Peter S.
 / TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
 / FILE REFERENCE: 0399.1192-008

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

```

Query Match      16.0%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
Db 1 KKGA 4

RESULT 39
US-09-746-742-18
; Sequence 18, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1998-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-18

Query Match      16.0%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
Db 1 KKGA 4

RESULT 40
US-09-984-245-297
; Sequence 297, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: PZ004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344

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; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 297
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-297

Query Match      16.0%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAAL 5
Db 1 MAAL 4

RESULT 41
US-09-996-634-94
; Sequence 94, Application US/09996634
; Patent No. US20020172684A1
; GENERAL INFORMATION:
; APPLICANT: Nano, Francis
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; FILE REFERENCE: 61260
; CURRENT APPLICATION NUMBER: US/09/996,634
; CURRENT FILING DATE: 2001-11-28

```

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

Acetylhydrolase

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/729,402
FILING DATE: 04-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 08/318,905
FILING DATE: 08-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. US20010021379Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-729-402-1

Query Match 16.0%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPRL 11
DB 14 LPRL 17

RESULT 44
US-10-117-846-46
Sequence 46, Application US/10117846
Patent No. US20020168673A1
GENERAL INFORMATION:
APPLICANT: Fuller, Margaret T
APPLICANT: Hales, Karen G.
APPLICANT: Santei, Ansgar H.
TITLE OF INVENTION: Microfusions, Fzo Homologs and Functional
FILE REFERENCE: STAN-063CIP3
CURRENT APPLICATION NUMBER: US/10/117,846
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/413,285
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: PCT/US00/27871
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-846-46

us-09-996-634-94

PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 94
LENGTH: 17
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-996-634-94

Query Match 16.0%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPRL 8
DB 8 LPRL 11

RESULT 42
US-09-996-634-95
Sequence 95, Application US/09996634
Patent No. US20020172684A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Immunostimulatory Peptides
FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 95
LENGTH: 17
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-996-634-95

Query Match 16.0%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPRL 8
DB 4 LPRL 7

RESULT 43
US-09-729-402-1
Sequence 1, Application US/09729402
Patent No. US20010021379A1
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor

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Query Match 16.0%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 RLJA 10
Db 14 RLJA 17

RESULT 45

US-09-864-761-39272
; Sequence 39272, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenshang
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aescmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39272
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004583.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EST_HUMAN HIT: AA832005.1, EVALUATE 7.00e-04
US-09-864-761-39272

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 LPRL 8
Db 9 LPRL 12

RESULT 46

US-09-746-742-17
; Sequence 17, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-17

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 21 KKGA 24
Db 3 KKGA 6

RESULT 47

US-09-746-742-19
; Sequence 19, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion

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```

FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
ID NO 19
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-19

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```

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 21 KKGa 24
Db 1 KKGa 4

```

```

RESULT 48
US-09-746-742-38
Sequence 38, Application US/09/746,742
Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-38

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```

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 21 KKGa 24
Db 1 KKGa 4

```

```

RESULT 49
US-09-746-742-39
Sequence 39, Application US/09/746,742
Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-39

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```

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 21 KKGa 24
Db 1 KKGa 4

```

```

RESULT 50
US-09-746-742-40
Sequence 40, Application US/09/746,742
Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30

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us-09-441-061-2.rapb

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```

PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-40

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 24
DB 1 KKG 4

RESULT 51
US-09-746-742-41
Sequence 41, Application US/09746742
Patent No. US2002007284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US 09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
NAME/KEY: VARIANT
LOCATION: (1)...(18)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-746-742-55

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 24
DB 1 KKG 4

RESULT 52
US-09-746-742-55
Sequence 55, Application US/09746742
Patent No. US2002007284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US 09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
NAME/KEY: VARIANT
LOCATION: (1)...(18)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-746-742-55

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 24
DB 1 KKG 4

RESULT 53
US-09-746-742-64
Sequence 64, Application US/09746742
Patent No. US2002007284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US 09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17

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Db 1 KKGa 4

RESULT 55
US-09-746-742-67
; Sequence 67, Application US/09746742
; Patent No. US2002007284A1
; GENERAL INFORMATION: Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-67

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGa 24
Db 1 KKGa 4

Search completed: December 19, 2002, 17:45:00
Job time: 11 secs

PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1998-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-64

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGa 24
Db 1 KKGa 4

RESULT 54
US-09-746-742-55
; Sequence 65, Application US/09746742
; Patent No. US2002007284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-65

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGa 24
Db 1 KKGa 4